SEARCH REQUEST FORM

Scientific and Technical Information Center

) Davis
Requester's Full Name:Phone ?	1	Examiner # :	Date:
Art Unit. Phone ? Mail Box and Bldg: Room Location	Number 30	Serial Number:	DARER DICK E MAI
Mail Box and Blog-Room Location	1: r	Cesting romnat rreferred (circi	el. PAPER DISK E-MAI
f more than one search is subm	nitted, please prio	ritize searches in order of	need. ********
Please provide a detailed statement of the Include the elected species or structures. I utility of the invention. Define any terms known. Please attach a copy of the cover.	keywords, synonyms, a that may have a specia	cronyms, and registry numbers, an il meaning. Give examples or relev	d combine with the concept or
Title of Invention:			
Inventors (please provide full names):			
•			
Earliest Priority Filing Date:			
For Sequence Searches Only Plcase inclu			d patent numbers) along with the
appropriate serial number.			,
	•		
		Jan (Jelaval .
		Biolechnology & CM i 1507 -	Journal Chemical Library 703-308-4498 Busplo.gov
STAFF USE ONE	Type of Search	Vendors and co	ost where applicable
Searcher Searcher	NA Sequence (#)		• •
Searcher Phone = 1449	AA Sequence (=)		
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Other

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STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 100105

TO: Phuong N Huynh Location: 8b13 / 9e12

Wednesday, July 30, 2003

Art Unit: 1644 Phone: 308-4844

Serial Number: 09 / 865198

From: Jan Delaval

Location: Biotech-Chem Library

CM1-1E07

Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

09/776,232 April 14.

Jan Delaval Reference Librarian Biotechnology & Chemical Library CM1 1E07 – 703-308-4498 jan.delaval@uspto.gov



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Delaval, Jan

From:

Huynh, Phuong N.

Sent:

Wednesday, July 30, 2003 8:44 AM

To: Subject: Delaval, Jan RE: RE: 09/865,198

Jan,

I would like to revise my search. Will you please just search peptide of 1-6, and 21-23 against commercial and interference databases? Thanks.

----Original Message-----

From:

Delaval, Jan

Sent:

Wednesday, July 30, 2003 8:37 AM

To: Subject: Huynh, Phuong N. RE: RE: 09/865,198

Neon -

The following sequences ARE NOT peptides: 9, 11-14, 24-26.

I will need authorization to process this request. Please obtain approval from one of the following examiners, and request that the approval be sent directly to me:

Martinell, Fredman, Priebe, P Tung, or M Pak.

Please do not submit multiple search requests.

I will wait for approval prior to processing this request.

Thanks.

Jan

----Original Message-----

From:

Huynh, Phuong N.

Sent:

Wednesday, July 30, 2003 8:26 AM

To:

Delaval, Jan

Subject: RE: 09/865,198

Jan,

Please search peptide of SEQ ID NO: 1-6, 9, 24, 11-14, 22-23 and 25-26 against commercial and interference databases.

Thanks, Neon Art unit 1644 Mail 9E12 Tel 308-4844

> Blotechnology & Chemical Library CMi 1E07 - 703-308-4498 jan.delaval@uspto.gov

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STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

	urnary Results reedback Form
>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	☐ Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	 Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
4	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Co	mments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 = Circ. Desk



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Result
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61.0	61.0	62.7	62.7	62.7	62.7	62.7	64.4	64.4	64.4	64.4	66.1	66.1	66.1	66.1
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Ig heavy chain V r	Ig heavy chain v r	. ਲ	Ig heavy chain VDJ		•	Ig heavy chain V r	conserved hypothet	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V-I	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V-V

ALIGNMENTS

Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculius (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S15672

RESULT 1 S15672

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A;Cross-references: EMBL:X73017
A;Experimental Bource: strain BALB/c
C;Superfamily: immunoglobulin V region; immunoglobulin h
C;Keywords: heterotetramer; immunoglobulin
F;15-40/Domain: immunoglobulin homology (fragment) <IMM>
                                                                                                                                                                                                                                                            R;Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
Eur. J. Immunol. 23, 206-211, 1993
A;Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes usin A;Reference number: S33391; MUID:93122092; PMID:8419173
A;Accession: S33408
                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change
C;Accession: S33408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: immunoglobulin V region; imm
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IV</pre>
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A;Accession: $15672
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA.
A;Molecule type: mRNA.
                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-40 < KET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, Bio/Technology 9, 266-271, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-116 <TEM>
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  Similarity 80.08; Conservative
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Similarity 90.0%; Pred. No. 0.0
9; Conservative 1; Mismatches
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                        88.1%;
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Pred. No. 0.0045;
2; Mismatches
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RESULT 5
S03482
    C; Accession; S
R; Rocca-Serra,
                 Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragm c;Species; Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence revision 26-Feb-1998 #text_change
C;Accession; S03482; S07453
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA; p
A;Residues: 1-114 <LES>
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A; Residues: 1-40, 'H'
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A;Accession: S36377
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Matches
                                                                                                                                                                                                                                                                                                                                                                                             ;Note: sequence extracted from NCBI backbone;Note: parts of this sequence were determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Lesley, S.A.; Patten, P.A.; Schultz, P.G. roc. Natl. Acad. Sci. U.S.A. 90, 1166, 1993 roc. Natl. Acad. Sci. U.S.A. 90, 1166, 1993 roc. Natl. Acad. Sci. U.S.A. 90, 1166 action of antibodies with enhanced catalytic act;Title: A genetic approach to the generation of antibodies with enhanced catalytic act;Reference number: A47271; MUID:93165660; PMID:8094556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Experimental source: strain BALB/c
;Superfamily: immunoglobulin V region; immunoglobulin homology
;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Title: Optimization of primers for cloning libraries of mouse;Reference number: S33391; MUID:93122092; PMID:8419173;Accession: S33392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g heavy chain V region - mouse (fragment)
;Species: Mus musculus (house mouse)
;Date: 19-Max-1997 #sequence_revision 29-Aug-1997 #text_change 23-Jul-1999
;Accession: S36377; S33392
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Matthes, H.W.;
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90.0%;
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Pred. No. 0.021;
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Pred. No.
Kaartinen,
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| by protein sequencing
Milstein,
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                                                                                                    mouse (fragment)
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C.; Theze,
                                        21-Jan-2000
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J.; Fougereau,
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A;Reference number: S03471;
A;Accession: S03471
A;Molecule type: mRNA
A;Residues: 7-120 <ROC1>
                                                                                                                                                                   Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text_change 20_Jun-2000
C;Accession: S03471; S07453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire A; Reference number: S07453; MUID:83058021; PMID:6815271 A; Accession: S07453
                                                                                  A_7 T it le: Analysis of antibody diversity: V-D-J mRNA nucleotide hypervariable regions.
                                                                                                                           R;Rocca-Serra, J.; Matthes, H.W.;
EMBO J. 2, 867-872, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-117 < MYL>
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C; Date: 22-Nov-1993
                                                                                                                                                                                                                                                                                 RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (E8) - mouse (fragment)
C; Species: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: this sequence was determined from the differentiated gene, R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 10-115 <ROC1>
A;Cross-references: EMBL:X03219
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Best Local :
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Similarity 90.0%;
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                                                                MUID:84057768;
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                                                                                                                                               Kaartinen, M.;
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Pred. No. 0
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0.022;
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                                                                                                                                                   Milstein,
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                                                                                                                                                 Theze, J.; Fougereau,
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C;Accession: S06823
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of
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S06823
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                 A;Reference number: S06815; MUID:90064531; A;Accession: S06823 A;Status: not compared with conceptual tran
                                                                                                                                                         Ig heavy chain V region (clone IIc) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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A;Variety: strain BALB/C
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03484; S07453
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A;Note: this sequence was determined from the differentiated gene
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A;Cross-references: EMBL:X07144
A; Molecule type: mRNA
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A;Accession: S03484
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Title: Analysis of antibody
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                   not compared with conceptual translation
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Pred. No.
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Pred. No. 0.022;
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Mismatches
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                                                                              murine monoclonal anti-morp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence of
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88
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-99/Domain: immunoglobulin homology <IMM>
RESULT 12
S49220
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                                                                                                                                                                                  A;Cross-references: EMBL:X57857; C;Keywords: immunoglobulin
                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-178 <SEY>
                                                                                                                                                                                                                                                              A; Reference number: S29593
A; Accession: S29594
                                                                                                                                                                                                                                                                                           R;Seymour, R. submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                     Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                            S29594
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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A; Residues: 1-123 <SHI>
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R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, J. Exp. Med. 176, 1209-1214, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (clone micro m- 46-6, 46-12) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
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Best Local
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Best Local
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                                                                             GFNIKDFYMH 10
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                                                             GFNI KDTYMH
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90.0%;
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Pred. No. 0.02
0; Mismatches
                                                                                                                                      Score 51;
Pred. No.
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Pred. No. 0.
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                                                                                                                                       DB 2;
0.034;
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0.023;
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0.023;
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Ig gamma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision

01-Aug-1997 #text_change 21-Jan-2000

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GFNI KDTYMH

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Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
(;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1956 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is function, Reference number: A56446; MUID:95229583; PMID:7713873
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A56446
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JC5322
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C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C;Accession: JC5322
C;Accession: JC5322
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A;Experimental source: strain Balb/c
C;Superfamily: immunoglobulin cregion; immunoglobulin homology
C;Keywords: immunoglobulin
C;Keywords: immunoglobulin
F;1-120/Domain: V region #status predicted <VRG>
F;1-121/Domain: C region #status predicted <CRG>
F;13'9-203/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-268 < TAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
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Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody targeted to A;Reference number: JC5322; MUID:97168950; PMID:9016757
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A; Residues: 1-221 < KIP>
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submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing
A;Reference number: S49220
                                                                                                                                                                                                                                                                                 A; Accession: A56446
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                                                                                       Query Match
Best Local S
                                                                                                                                                               Keywords: heterotetramer;
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Best Local s
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Best Local Similarity 90.0%;
Matches 9; Conservative
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                                                                                                                                                                                     Cross-references: GB:U20617
                                                                                                                                                                                                                                                              Status: preliminary
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GENIKDEYMH 10
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                                                                      Similarity 90. 9; Conservative
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                                                                                            90.0%;
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                                                                                                                                                          immunoglobulin
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                                                                   Score 51; DB 2;
Pred. No. 0.052;
0; Mismatches
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Pred. No. 0.045;
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Pred. No. 0.042;
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                                                                                                                 Length 268;
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                                                                      Indels
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Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revisior
C;Accession: S16028
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;KeyWordds: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Tutter, A.; Brodeur, P.; Shlomchik, M.; Riblet, R.
submitted to the EMBL Data Library, September 1990
A;Description: Structure, Map position, and evolution of two newly diverged mouse immuno
Search completed: July 30, 2003, 09:44:03 Job time : 3.95681 secs
                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-97 < TUT>
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S16028
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                                                                                                                                                                                Query Match
Best Local S
Matches 9
                                                                                                                                                                             Local Similarity
tes 9; Conserv
                                                                                         25
                                                                                                                                    1 GFNIKDFYMH 10
                                                                                                                                                                                    Conservative
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                                                                                         34
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                                                                                                                                                                                Score 50; DB 2;
Pred. No. 0.027;
0; Mismatches
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Result
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Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 su
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                                                                                                                                                                                                                                                    35.5
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.
carboxykinase) (Phosphoenolpyruvate carboxylase) (PCKG OR TA0123.
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DOMAIN 1 114 IG-LII
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-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-!- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CA
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Nature 291:29-34(1981)
-I- MISCELLANEOUS: THIS CHAIN WAS
BINDS PHOSPHORYLCHOLINE.
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Similarity 7; Conserv

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MEDITINE-92114084; PubMed=1731088;

Wolfe K.H., Morden C.W., Palmer J.D.;

Wolfe K.H., Morden C.W., Palmer J.D.;

"Small single-copy region of plastid DNA in the non-photosynthetic

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EMBL; M81884; AAA65870.1; --
PIR; S20614; S20614.
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"Function and evolution of a minimal plastid genome nonphotosynthetic parasitic plant.";
Proc. Natl. Acad. Sci. U.S.A. 89:10648-10652(1992).
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bioenergetic locus.";
J. Mol. Biol. 223:95-
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Asteridae; lamiids; Lamiales; Orobanchaceae; Orobancheae; Epifagus
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28-FEB-2003
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Pfam; PF00821; PEPCK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93066301; PubMed=1332054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: NOT YET KN
SIMILARITY: BELONGS
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Pred. No.
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SEQUENCE OF 1-120.
MEDLINE-75017346; PubMed=4213527;
Rudikoff S., Potter M.;
"Variable region sequence of the heavy
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21-JUL-1986
15-SEP-2003
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P01789;
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
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PIR; B90795; AVMS63.
                                                                                                                                                                                                                                                                                                                             Proc.
                                                                                                                                                                                                                                                                                                                                                                                                        binding myeloma protein.";
Biochemistry 13:4033-4038(1974).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=80199926; PubMed=6769593;
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Mammalia; Eutheria;
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MEDLINE=75065510; PubMed=4530984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                         PROSITE
                                                                                                                                                                                                mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heavy chain
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SIMILARITY: Contains 1 immunoglobulin-like domain.
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2MCP; 15-JUL-92.
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,0047; ig; 1.

,000406; IGV; 1.

,000406; IG LIKE; 1

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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
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Rodentia;
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H-BOND WITH THE
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RESULT 6
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   RRR OCC OCT DT AC
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21-JUL-1986 (Rel. 01, Last seq
21-SEP-2003 (Rel. 42, Last anr
15-SEP-2003 (Rel. 42, Last anr
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Mammalia; Eutheria; Rodentia;
                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
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SMART; SM00406; IGv;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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(MOPC 511).";
Proc. Natl. Acad.
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SEQUENCE (TEPC 15).
MEDLINE=76222762; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROSITE; PS50835; IG_LIKE; mmunoglobulin V region.
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I- SIMILARITY;
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116
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Pred. No. 9.1;
0; Mismatches
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                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local S
Matches 6
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21-JUL-1986
21-JUL-1986
15-SEP-2003
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SEQUENCE
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MEDLINE=8019926; PubMed=6769593;

Early P., Huang H., Davis M., Calame K., Hood L.;

"An immunoglobulin heavy chain variable region gene is three segments of DNA: VH, D and JH.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rudikoff S., Potter M.; "Size differences among immunoglobulin heavy chains "Size differences among immunoglobulin heavy chains phosphorylcholine-binding proteins."; proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rudikoff S., Barstad P., Potter M., Hunpublished results, cited by:
Hood L., Campbell J.H., Elgin S.C.R.,
Annu. Rev. Genet. 9:305-353(1975).
                                                 -!- SIMILARITY: Cor
HSSP; P01789; 1MCP.
                                                                                           Barstad P.;
Thesis (1975),
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                               Ig heavy chain V region H8. Mus musculus (Mouse).
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma.
Immunoglobulin V region; Hybridoma.
Immunoglobulin V region; Hybridoma.
Ill IG-LIKE.
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                           InterPrp;
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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InterPro; IPR003006;
InterPro; IPR003596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     their IgM counterparts."; Nature 291:29-34(1981).
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    IPR003006;
                             IPR007110;
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123 AA;
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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
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                                                                       Contains 1 immunoglobulin-like domain
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Ig_MHC.
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Ig-like
Ig_MHC.
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Pred. No. 9.
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                                                                                                                    e of Technology
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MYELOMA PROTEIN
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PEam; PR00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1
Temnoglobulin V region.
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P01792;
21-JUL-1986
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P01791;
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SMART; SMO0406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma.
nomain 1 114 IG-LIKE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosgomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=81197602; PubMed=7231520;
Gearhart P.J., Johnson N.D., Douglas R., Hood
"IgG antibodies to phosphorylcholine exhibit m
their IgM counterparts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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21-JUL-1986 (Rel.
15-SEP-2003 (Rel.
                      Eukaryota; Metazoa;
                                                                Ig heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 291:29-34(1981)
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IPR003596; Ig_v.
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123 AA;
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123 AA;
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                                                                  (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
ain V region HPCG8.
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                              region HPCG8
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01, Last sequence update)
42, Last annotation update)
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66.7%;
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Pred. No.
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Pred. No.
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Sciurognathi; Muridae; Murinae; Mus
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Best Local
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P01795;
21-JUL-1986
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HSSP; P01789; IMCP.
InterPro; IPR0031006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
"IgG antibodies to phosphorylcholine exhibit more diversit
their IgM counterparts.";
Nature 291:29-34(1981).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA
BINDS PHOSPHORYLCHOLINE.
                                                                                          use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      "Size differences among immunoglobulin heavy chains from phosphorylcholine-binding proteins.";
Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93358330; PubMed=6101208; Kim S., Davis M., Sinn E., Patten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region M167 precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Hybridoma.
Immunoglobulin V 114 IG-LIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
                         EMBL; J00516; AAC18867.2; ALT_TERM PIR; A90818; AVMS67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rudikoff S., Potter M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 20-142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=76222762; PubMed=819932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Antibody diversity: somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL
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66.7%;
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Pred. No.
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hypermutation
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                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                   There are no restrictions ng as its content is in
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                                                                                                                                              Usage
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RESULT 12
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                           RC TISSUE=Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toeshyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toeshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Women R. D. Inckson M. C.
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Best Local S
Matches 6
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SEQUENCE FROM N.A.
MEDLINE=98287625; PubMed=9624529;
MEDLINE=98287625; PubMed=9624529;
Magata M., Suzuki M., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Serpin I2 precursor (Mycepithelium-derived se
(Pancpin) (Protease inhibitor 14) (TSA2004).
SERPINI2 OR PI14 OR MEPI.
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CONFLICT
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SEQUENCE
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CHAIN
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                     "Suppression of breast cancer growth and metastasis by a serpin myoepithelium-derived serine proteinase inhibitor expressed in the mammary myoepithelial cells.";
Proc. Natl. Acad. Sci. U.S.A. 96:3700-3705(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ozaki K., Nagata M., Suzuki M., Fujiwara T., Miyoshi Y., Ishikawa O., Ohigashi H., Imaoka S., Takahashi E., Nakamura Y.; "Isolation and characterization of a novel human pancreas-specific gene, pancpin, that is down-regulated in pancreatic cancer cells."; Genes Chromosomes Cancer 22:179-185(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    075830;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99199247; PubMed=10097100; Xiao G., Liu Y.E., Gentz R., Sang
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                     Touchman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53
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                    J.W.,
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Pred. No. 11;
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IG-LIKE.
N -> D (IN REF. 2).
     Schmutz
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                  Green
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                     E.D., Dickson M.C.
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full human and mouse cDNA sequences.";

15,000 full-length

D.E.,

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RESULT 13
IRK4_CAEEL
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Matches
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P52192;

01-OCT-1996 (Rel. 34, Create

01-OCT-1996 (Rel. 34, Last s

16-OCT-2001 (Rel. 40, Last a

Inward rectifier potassium c
                                          Wilcox L.;
Submitted (NOV-1995) t
Submitted (NOV-1995) t
-i- FUNCTION: INWARD R
-i- GREATER TENDANCY I
THAN OUT OF IT.
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CARBOHYD
SEQUENCE
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ACT_SITE
CARBOHYD
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Serpin; S
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- SUBCELLULAR LOCATION: Secreted (Probable).

-!- TISSUE SPECIFICITY: Expressed in pancreas and acade of the control of the serpin family.
                                                                                                                                                Caenorhabditis elegans
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                    SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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SMART; SM00093; SERPIN; 1.
                                                                                                                                     NCBI_TaxID=6239;
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GO:0008181; F:tumor suppressor;
GO:0006928; P:cell motility; TAS.
erPro; IPR000215; Serpin.
                    SUBCELLULAR LOCATION SIMILARITY: BELONGS
         FAMILY.
                                                                                                                                                                                                                                                         CAEEL
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605587; -.
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; AAD34723.1; -.
; AAH27859.1; -.
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                                LOCATION: Integral
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Caenorhabditis.
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Pred. No. 30;
3; Mismatches
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SERPIN 12.
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irk-4.
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Matches 5
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Peterson J., DeBoy R., Dodson
Kolonay J.F., Nelson W.C., Uma
Delcher A., Utterback T., Weid
Bishai w
                                                                                                                                                                                                                       MEDLINE-98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.",
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
SEQUENCE
                  Bishai W.; "Whole genome comparison
                                                                                                                                  STRAIN=CDC 1551 / Fleischmann R.D.,
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MEDLINE=98295987;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32)
carboxykinase) (Phosphoenolpyruvate carboxylase) (PE)
PCKG OR PCKA OR PCKI OR RV0211 OR MT0221 OR MTCY08D5
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                                                                                                                                                                               SEQUENCE
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
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InterPro; IPR001838; K+channel_IR.
InterPro; IPR001622; K+channel_pore.
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PIR; T28859; T28859
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                                                           D., Eisen J.A., Carpenter dson R., Gwinn M.L., Haft, Umayam L.A., Ermolaeva Weidman J., Khouri H., G
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                                                               Carpenter L., White O.,
M.L., Haft D., Hickey E.,
Ermolaeva M.D., Salzberg
ouri H., Gill J., Mikula
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Best Local
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                                                                                                                                                                                                                                                                                              CRAR HUMAN STANDARU;
P48740; O95570; Q9UF09;
11-FEB-1996 (Rel. 33, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Complement-activating component of Ra-reactive factor precursor (EC 3.4.21.-) (Ra-reactive factor serine protease p100) (RaRF)
(Mannan-binding lectin serine protease 1) (Mannose-binding protease)
(MASP-1).
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PROSITE; PS00505; PEPCK_GTP; 1.

Gluconeogenests; Lyase; Decrabox/lase; GTP-
NP_BIND 222 229 GTP (POTENTIAL
ACT_SITE 273 273 BY SIMILARITY.

SECUENCE 606 AA; 67253 MM; AEE29412E6BC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               MEDIINE=94289349; PubMed=8018603;
Sato T., Endo Y., Matsushita M., Fujita T.;
"Molecular characterization of a novel serine protease involved activation of the complement system by mannose-binding protein."
                                                                                                                     MEDLINE=94059062; PubMed=8240317;
Takada F., Takayama Y., Hatsuse H., Kawakami M.;
"A new member of the C1s family of complement proteins f
bactericidal factor, Ra-reactive factor, in human serum.
Biochem. Biophys. Res. Commun. 196:1003-1009(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF_00452; -; 1.
InterPro; IPR000364; PEP_carboxykin.
Pfam; PF00821; PEPCK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z92669; CABO7006.1; -- . EMBL; AE006931; AAK44442.1; -- . PIR; A70960; A70960. TIGR; MT0221; -- .
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                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TubercuList; Rv0211; -.
                                                                                           SEQUENCE
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SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Monomer (By a SUBCELLULAR LOCATION: SIMILARITY: BELONGS TO
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Pred. No. 45;
4; Mismatches
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EMBL; D28593; BAA04864.1; JOINED
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EMBL; AB010813; BAA34864.1; JOINED
EMBL; AB010814; BAA34864.1; JOINED
EMBL; AB010816; BAA34864.1; JOINED
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EMBL; AB010818; BAA34864.1; JOINED
EMBL; AB010819; BAA34864.1; JOINED
EMBL; AB010820; BAA34864.1; JOINED
EMBL; AB010821; BAA34864.1; JOINED
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EMBL; AB007616; BAA89206.1; JOINED
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MOL. IMMUDOL. 36:505-514(1999).

MHICH SPECIFICALLY BINDS TO RA AND R2 POLYSACCHARIDES EXPRESSED CHARLAN SPECIFICALLY BINDS TO RADIONENTS. THE ACTIVATION OF COMPLEMENT CHARLAN IN THE ACTIVATION OF COMPLEMENT CHARLAN IN THE ALPHA-CHAIN OF C4.

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CICASCADE BY ACTIVATION OF A COMPLEMENT-ACTIVATING COMPONENT (CEARF) AND A POLYSACCHARIDE-BINDING (MANNOSE-BINDING) COMPONENT (CEARF) AND A POLYSACCHARIDE-BINDING (MANNOSE-BINDING) COMPONENT CRAFF IS AN HETERODIMER OF A HEAVY (P70) AND A LIGHT CHAIN (P29) LINKED BY A DISULTIDE BOND.

-I- DOMAIN: CRARF HAS A MODULE ORGANIZATION SIMILAR TO C1R AND C1S.

-I- SIMILARITY: Contains 2 Sushi (SCR) domains.

-I- SIMILARITY: Contains 2 CUB domains.

-I- SIMILARITY: Contains 2 CUB domains.
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Takayama Y., Takada F., Nowatari M., Kawakami M., Mats "Gene structure of the P100 serine-protease component reactive factor.";
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Exon structure of the gene encoding the human mannose-binding protein-associated serine protease light chain: comparison with complement C1r and C1s genes.", Int. Immunol. 8:1355-1358(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97079701;
Endo Y., Sato T.,
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Matsushita M.,
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MIM; 600521;
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001859; CUB domain.
R InterPro; IPR001861; EGF_Cas.
R InterPro; IPR00186209; EGF_like.
R InterPro; IPR001254; Ser_protease_TINterPro; IPR001254; Ser_protease_TINTERPRO; Sushi_SCR_CCP.
DR Pfam; PF000431; CUB; 2.
DR Pfam; PF00084; sushi; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00089; CHYMOTRYPSIN.
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SMART; SM00032; CCP; 2.
SMART; SM00032; CCP; 2.
SMART; SM00042; TCYP; 2.
SMART; SM000179; EGF_CA; 1.
SMART; SM00020; TTYP; SPC; 1.
PROSITE; PS001180; CUB; 2.
PROSITE; PS01180; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
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MEROPS; S01.198; -.
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Repeat; Signal; EGF-like domain; Hydroxy
9 POTENTIAL.
9 COMPLEMENT-ACTIVATING COMPONENT
RA-REACTIVE FACTOR.
8 70 kDa CHAIN OF P100 (P70).
9 29 kDa CHAIN OF P100 (P29).
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EGF-like domain; Hydroxylation.
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sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                       sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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Q9j185 mus musculu
Q9j131 mus musculu
Q8j1jd7 plasmodium
Q8esf8 oceanobacil
Q8es25 leptospira
Q9f737 uncultured
Q8ryq7 oryza sativ
Q1321 metarhizium
Q8ga98 synechococc
Q9prd1 ureaplasma
Q8iinz plasmodium
Q8d2m7 wiggleswort
Q979c1 thermoplasm
Q9mix6 uroleucon r
Q9mix6 uroleucon s
Q9mix4 uroleucon r
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59.3			•				59.3		•	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	•		61.0	•	61.0	•	۲	61.0	۳	61.0
399	389	365	319	316	279	252	170	156	6629	2763	791	733	733	728	719	646	600	570	521	488	385	372	369	309	309	309	225	222
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Q9F0P1	Q9MJ75	Q8R695	Q8VWY2	Q8II10	Q9BQG8	Q9H9F2	020625	020623	Q91QT2	Q8I3X5	Q22142	Q8CD27	Q920S0	Q96RS4	Q9PVY2	097132	Q8RY84	TQY16D	Q84358	QBIUVB	Q8FPC3	Q8MT70	Q8NP54	Q8E0Q9	Q8E6C7	Q9X432	034769	Q97XU3
		Q8r695 fusobacteri		ъ	Q9bqg8 homo sapien		O20625 physarum po		Q91qt2 avian infec	Q8i3x5 plasmodium	caen	Q8cd27 mus musculu	Q920s0 mus musculu	homo sapi	Q9pvy2 triakis scy	O97132 drosophila	Q8ry84 arabidopsis		Q84358 mastomys na	₽	Q8fpc3 corynebacte	Ω.			Q8e6c7 streptococc	Ø	O34769 bacillus su	Q97xu3 sulfolobus

ALIGNMENTS

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GFNIEDTYMH

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RESULT 3
Q81JJ 10
Q81JJ 20
ID Q81J
D7 01-M
D7 01-M
D7 01-M
D7 01-M
D7 01-M
D7 01-M
D8 Hypo
GN PF100
OS P1as
OX NCB1
RN [1]
RN [1]
RN [1]
RR SEQU
RC STRA
RX MEDL
RA Gard
RA Carl
RA Carl
RA Carl
RA Pert
RA MART
RA MCFa
RA Vent
RA MATU
RA Fras
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Q99L31
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Pfam; PF00047; 19; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

PROSITE; PS00290; IG_MHC; 1.
                                                                                                  MEDLINE=22255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.,
Fraser C.M., Barrell B.,
France sequence of the human malaria parasite Plasmodium
                                              Nature 419:498-511(2002).
EMBL; AE014833; AAN35458.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                            Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=36329;
                                 SEQUENCE
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01-MAR-2003
                                                                                          falciparum."
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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P01842; 7FAB.
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(TrEMBLrel.)
(TrEMBLrel.)
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                             71631 MW;
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Apicomplexa; Haemosporida; Plasmodium.
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Last sequence update)
Last annotation updat
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Pred. No.
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                              2D178B275234A75C CRC64;
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   43;
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n S., Paulsen I.T., James K.,
Craig A., Kyes S.,
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RESULT 5
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Q8ESF8
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Best Local S
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Best Local S
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Q8EZ25;
01-MAR-2003
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01-MAR-2003
01-MAR-2003
                                                                                 EMBL; AE011558; AAN51234.1;
Helicase; Complete proteome
SEQUENCE 948 AA; 110694
                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, ATP-dependent RNA helicase.
                                                                                                                   Submitted (MAR-2002) to the
                                                                                                                             Ren S.;
                                                                                                                                       STRAIN=56601 /
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                               Leptospira interrogans.
Bacteria; Spirochaetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-2220767; PubMed-12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from
Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. OB0681.
                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein;
SEQUENCE 156 AA; 17
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EMBL; AP004595; BAC12637.1; -.
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STRAIN=HTE831 / DSM 14371 / JCM 11309;
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Bacteria; Firmicutes; Bac
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                                                                                                                                                                     CBI_TaxID=173;
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FNLODYYSH
                    FNIKDFYMH 10
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948 AA; 110694 P
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677
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17548 MW;
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55.6%;
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                                                                                                                                                                                Spirochaetales; Leptospiraceae;
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23,
                                                                                 MW;
                                        Score 38; DB
Pred. No. 2.3e
3; Mismatches
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4B784980F816C301 CRC64;
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annotation updat
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RESULT 7
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Matches 6
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STRAIN-cv. Nipponbare;
STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T. Yamamoto K.;
"Oryza sativa (japonica cultivar-group) ge
clone:OSJNBA005JH17.";
Submitted (OCT-2001) to the EMBL/GenBank/I
-i- SIMILARITY: BELONGS TO THE CYTOCHROME
EMBL; AP004232; BAB90702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8RYQ7
Q8RYQ7;
01-JUN-2002
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Q9F7$7;
Q9F7$7;
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                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                         InterPro; IPR001128; Cytochrome Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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OSJNBA0051H17.12.
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Pfam; PF00557; Peptidase_M24; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF279106; AAG10442.1; -. HSSP; P15034; 1A16.
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01-MAR-2001 (TrEMBLrel. 16, Last
01-DEC-2001 (TrEMBLrel. 19, Last
Predicted Xaa-Pro aminopeptidase.
                                                                                                                                                                                                                                                                                                                                                                       Gramene; Q8RYQ7;
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Jovanovich S.B., Gates C.M., Fel
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NCE 497 AA;
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                                                                                                                        Conservative
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   228
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56136 MW; E18FB1E625DBC672 CRC64;
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, Feldman
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Pred. No.
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man R.A., Spu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Embryophyta; Tracheophyta;
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RESULT 9
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Best Local :
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01-DEC-2001 (TrEMBLrel. 19, Las
Proline rich protein 5MeD.
Metarhizium anisopliae.
Bukaryota, Fungi; Ascomycota; Probkaryota; Fungi; Ascomycota; Prypocreales; Clavicipitaceae; m. NCBI TaxII-5530;
                                                                                                                 Lyase.
SEQUENCE
                                                                                                                                                          Holtman C.K., Sandoval P., Chen Y., Socias T., McMurtry S., Gonzalez A., Salinas I., Golden S., "Synechooccus elongatus PCC 7942 cosmid 3E9 "; submitted (JUL-2002) to the EMBL/GenBank/DDBJ d
                                                                                                                                                                                                                                                              SEQUENCE OF 1-268 FROM N.A.
MEDLINE=20026086; PubMed=10556522;
MILLER B., Heuser T., Zimmer W.;
MILLER B., Heuser T., Zimmer W.;
"A Synechococcus leopoliensis SAUG 1402-1 operon harboring the deoxyxylulose 5-phosphate synthase gene and two additional open reading frames is functionally involved in the dimethylallyl diphosphate synthesis.";
                                                                                                                                                                                                                                                                                                                                                                                              Synechococcus sp. (strain PCC 7942) (Anacystis nidular Bacteria; Cyanobacteria; Chroococcales; Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metarhizium anisopliae.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF012440; AAB69315.1;
SEQUENCE 534 AA; 55702 MW; C1442431B7E15043 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Joshi L., St Leger R.J., Roberts "Identification and isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ARSEF2575;
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                                                                                                                                            EMBL; X04616; CAD55648.1; -.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                       Similarity 5; Conserv
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3 (TrEMBLrel. 05,
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5h protein 5MeD.
                                                                                                                 542 AA;
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                                                                                                                 59000 MW;
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Last annotation update)
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Pred. No.
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differentially
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                                                                                  Length 542
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RESULT 11
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01-MAR-2003 (TEMBLrel. 15, Last sequence update)
01-MAR-2003 (TEMBLrel. 23, Last annotation update)
Ribose/galactose ABC transporter (N-term domain).
RBSC-1 OR UU014.
                                                                                                                                                 MEDLINE=22255705; PubMed=12368864;
Gardner M.J., Hall N., Fung B., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; Prozecome.
Complete proteome.
736 AA;
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MEDLINE=20500219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE002101; AAF30419.1; -.
InterPro; IPR001851; Bac_inmem_transp
Pfam; PF02653; BPD_transp_2; 1.
                                                                               Hypothetical protein.
SEQUENCE 5922 AA; 710211 MW;
                                                                                                   Nature 419:498-511(2002).
EMBL; AE014837; AAN35722.1; -.
                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glass J.I., L. Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma
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01-OCT-2000
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                                                                                                                                                                                                                                                                   STRAIN=3D7
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                               Q8IIN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 407:757-762(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     urealyticum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=134821;
                                                                                                                                       Genome sequence of the human malaria parasite Plasmodium
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5; Conserv
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(TrEMBLrel.
(TrEMBLrel.
                                   Conservative
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55.6%;
                                             62.7%;
                                                                                                                                                                                                                                                                                                                  Apicomplexa; Haemosporida; Plasmodium
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                                                                                                                                                                                                                                                                                                                                                               23,
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Last sequence update)
Last annotation updat
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                                             Score 37;
Pred. No.
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Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33872F58F29B6EB3 CRC64;
                                  Mismatches
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                                             DB 5; L
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Q979C1;
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Q8D2M7;
01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                STRAIN-GSS1 / DSM 4299 / JCM 9571;

MEDLINE-20570466; PubMed=11121031;

Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,

Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., K.

Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.

"Archaeal adaptation to higher temperatures revealed by gen

sequence of Thermoplasma volcanium.";

Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

EMBL; AP000995; BAB60382.1;

TENEST. ITTOCOCOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT 2001 (TrEMBirel 18, C
01-OCT-2001 (TrEMBirel 18, I
01-MAR-2002 (TrEMBirel 20, I
N-terminal acetyltransferase
                                                                                                                                                      InterPro; IPR000182; GCN5acetyltransf
Pfam; PF00583; Acetyltransf; 1.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                     Thermoplasma volcanium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             flies, Wigglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002).
EMBL; AB063522; BAC24473.1; -.
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Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wigglesworthia brevipalpis.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
                                                                                                                                         Transferase;
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                                                            Similarity 6; Conserv
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GFNIKEFIVN
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50 AA; 17571 MW;
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e complex subunit.
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3; Mismatches
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Pred. No. 1
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Q9MIX6;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
NADH dehydrogenase subunit 1 (EC 1.6.5.3) (NADH-ubiquinone
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SEQUENCE
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NAD; C
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Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Uroleucon.
NCBI_TaxID=87321;
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01-OCT-2000 (TrEMBLrel. 25, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
NADH dehydrogenase subunit 1 (EC 1.6.5.3) (NADH-ubiquinone
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Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Uroleucon.
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Uroleucon rudbeckiae.
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                                            Oxidoreductase; Transmembrane; Ubiquinone; Mitochondrion.
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                                                                      Pro; IPR001694; Resp_NADH_dh1.
PF00146; NADHdh; 1.
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22120 MW;
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                                Similarity 5; Conserv
FNLNDFYIY 131
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                                        Score 36; DB 8;
Pred. No. 1e+02;
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Result
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                      Score
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Match Length DB
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1: /cgn2_6/ptodata/1/pubpaa/PCT
2: /cgn2_6/ptodata/1/pubpaa/PCT
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/ Cgm2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
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_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
US-09-976-787-7

US-09-976-787-23

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US-09-976-787-29

US-09-976-787-28

US-09-976-787-28

US-09-976-787-28

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US-09-798-689-1
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Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 23, Appl
Sequence 22, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 28, Appl
Sequence 28, Appl
Sequence 21, Appl
Sequence 28, Appl
Sequence 27, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                      Description
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-1
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Patent No. US20020064528A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping)
APPLICANT: Witte, Larry
APPLICANT: NVENTON: Antibodies Specific to
FILE REFERENCE: 11245/46505
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 1
                                                                                                                                                                                                                                          Matches
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equence 5,	e 4,	equence 3,	e 2,	e 1,	e 12,	e 11,	e 10,	e 9,	e 8	e 7,	equence 6,	e 5	e 4,	e 3,	equence 2,	e 1,	e 12,	e 11,	e 10,	e 9,	•	equence 7,	e 6,	e 5,	4,	Sequence 3,	2,	μ	1,
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ALIGNMENTS

KDR and Uses Thereof

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RESULT 2

US-09-865-198-1

; Sequence 1, Application US/09865198

; Patent No. US20020103345A1

; GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: Zhu, Zhenping
                                                                                                                                        GENIKDFYMH 10
                                                                                                                      GFNIKDFYMH 10
                                                                                                                                                                               Conservative
                                                                                                                                                                                             100.0%; Score 59; DB 9; 100.0%; Pred. No. 9.8e-05;
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; ORGANISM: Mouse
US-09-865-198-1
                                                               Sequence,7, Application US/09976787 Patent No. US20020064528A1 GENERAL INFORMATION:
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Matches
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LENGTH: 1
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Publication No. US20030103973A1
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Best Local Similarity
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TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
                           APPLICANT: Zhu, Zhenping APPLICANT: Witte, Larry
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PRIOR APPLICATION NUMBER: 08/
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PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
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CURRENT FILING DATE: 2001-05-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and MethorITLE OF INVENTION: Production
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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T: Witte, Larry INVENTION: Antibodies Specific to KDR and Uses Thereof
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Pred. No.
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; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23
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Best Local Similarity
Marches 10; Conserva
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LENGTH: 117
TYPE: PRT
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 7
                                                                                                                               GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
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                                                                                                                                                                                                                             Sequence 7, Application US/09865198 Patent No. US20020103345A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                     CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
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CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to
FILE REFERENCE: 11245/46505
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Pred. No. 0.0013;
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Pred. No.
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PRIOR APPLICATION NUMBER: 08/706,804
PRIOR FILING DATE: 1996-0-3
PRIOR FILING DATE: 1996-0-03
PRIOR APPLICATION NUMBER: 08/476,533
PRIOR APPLICATION NUMBER: 08/326,552
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/326,552
PRIOR PILING DATE: 1994-10-20
08/196,041
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US-09-798-689-7
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; ORGANISM: Mouse
US-09-865-198-22
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US-09-865-198-22
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; ORGANISM: Mouse
US-09-865-198-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 22
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methd
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
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Patent No. US20020103345A1
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Best Local Similarity
NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
SEQ ID NO 7
LENGTH: 117
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/401,165
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 08/967,113
PRIOR APPLICATION NUMBER: 1997-11-10
PRIOR PILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                 APPLICANT: Goldstein, Neil I.

TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined with Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
DEFICE APPLICATION NUMBER: 06/401-163
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                                                                               PRIOR APPLICATION I
                                                              APPLICATION NUMBER: 08/1
A APPLICATION NUMBER: 08/1
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                                           PatentIn Ver. 2.1
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Pred. No. 0.0013;
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Pred. No. 0.0013;
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; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29
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US-09-976-787-29
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US-09-865-198-28
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                                                                                                                                    US-09-865-198-28
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APPLICANT: Zhu, Zhenping
APPLICANT: InvENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 28
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Best Local Similarity
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Patent No. US20020103345A1
                                                                                  Best Local Similarity
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APPLICANT: Witte, Larry
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/99/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILLING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
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                                                                                                                                                     TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                     LENGTH: 238
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Local Similarity 100.0%;
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                                1 GFNIKDFYMH 10
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GFNIKDFYMH
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nilarity 100.0%;
Conservative 0
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                                                                100.0%; Score 59; DB 10
100.0%; Pred. No. 0.0027,
Live 0; Mismatches (
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Pred. No. 0.0013;
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                                                                                                  DB 10;
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                                                                                                  Length 238;
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; SOFTWARE: WordPer
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28
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APPLICANT: Witte, Larry
APPLICANT: Witte, Larry
FITLE OF INVENTION: Antibodies Specific to KDI
FILE REPERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
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US-09-976-787-28
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; ORGANISM: Mouse
US-09-798-689-21
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SOFTWARE: Par
; SEQ ID NO 21
FRIGHT: 238
                                                                            Matches
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Best Local Similarity
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Best Local Similarity
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PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 08/9
PRIOR FILING DATE: 1997-11-10
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APPLICANT: Goldstein, Neil I.

TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined with Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CÜRRENT APPLICATION NUMBER: US/09/798,689

CÜRRENT FILING DATE: 2001-03-02

CÜRRENT FILING DATE: 2001-03-02
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PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1996-09-03
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                                    1 GENIKDFYMH 10
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  26 GFNIKDFYMH
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                                                                                        100.0%;
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                                                                                          Score 59; DB 9;
Pred. No. 0.0027;
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                                                                                                              Length 240;
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Best Local Similarity
Thehes 10; Conserve
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                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/032,482
CURRENT FILING DATE: 2002-01-02
PRIOR APPLICATION NUMBER: US/09/445,602
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: PCT/IL98/00266
PRIOR APPLICATION NUMBER: L1 121041
PRIOR APPLICATION NUMBER: I1 121041
PRIOR FILING DATE: 1997-06-09
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SEQ ID NO 7
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APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
                                                                                                  Query Match
Best Local
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APPLICANT: Cohen, Irun
APPLICANT: ROTTER, Vai
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Publication No. US20020197270A1
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HERKEL, Johannes
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION
TITLE OF INVENTION: IMMUNITY
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                          LENGTH: 112
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: COHEN42
                                                                   1 Docal Similarity 90.0%; hes 9; Conservation
  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                    1 GENIKDFYMH 10
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                                                                                                                                                                                                                                                         PatentIn version 3.0
||||||:|||
GFNIKDYYMH 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wolkowicz, Roland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROTTER, Varda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EREZ-ALON, Neta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RUIZ, Pedro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 59; DB 10; ilarity 100.0%; Pred. No. 0.0027; Conservative 0; Mismatches 0
                                                                             Score 56; DB 14; Length 112; Pred. No. 0.0044; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 240;
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RESULT 15 US-09-802-083-1

Sequence 1, Application US/09802083 Publication No. US20030119075A1

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GENERAL INFORMATION:

APPLICANT: Kirchhofer, Daniel K.

APPLICANT: Lowe, David G.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Anti-Tissue Factor Antibodies with Enhanced TITLE OF INVENTION: Anti-Oagulant Potency

FILE REFERENCE: P136R1

CURRENT FALING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: US/09/802,083

CURRENT FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: US 60/189,775

PRIOR APPLICATION NUMBER: US 60/189,775

PRIOR FILING DATE: 2000-03-16

NUMBER OF SEQ ID NOS: 28

SEQ ID NO 1

LENGTH: 117

TYPE: PRT

ORGANISM: Mus Musculus

US-09-802-083-1

Query Match

Best Local Similarity 90.0%; Pred. No. 0.0466;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ORGANISM: Search completed: July 30, 2003, 10:20:28

Search completed: July 30, 2003, 10:20:28
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Sequence
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Sequence Sequence Sequence Sequence Sequence

10, Appl 12, Appl 4, Appl 6, Appl 31, Appl 31, Appl 31, Appl 31, Appl 31, Appl 31, Appl 32, Appl 32, Appl 32, Appl 33, Appl 34, Appl 35, Appl 36, Appl 37, Appl 38, Appl 39, Appl 31, Appl 31, Appl 31, Appl 31, Appl 32, Appl 33, Appl 34, Appl 35, Appl 36, Appl 37, Appl 38, Appl 39, Appl 30, Appl 31, A

Sequence Sequence Sequence Sequence

Sequence

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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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59
1 GFNIKDFYMH 10
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131.295 Million cell updates/sec
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Gapop 10.0 ,
  Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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  GenCore version (c) 1993 - 2003
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            US-08-732-708C-43
US-08-737-708C-43
US-08-017-570-6
US-08-017-570-6
US-08-471-426-6
US-09-672-609-1
US-09-672-609-5
US-09-672-609-6
US-09-672-609-7
US-09-672-609-7
US-09-672-609-7
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US-09-672-609-1
US-09-672-609-1
US-09-672-609-1
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US-09-672-609-1
US-09-672-609-1
US-09-672-609-1
US-09-672-609-1
US-09-025-403A-3
US-09-025-403A-3
US-09-025-403A-5
US-09-025-403A-6
US-09-025-403A-6
US-09-025-403A-6
US-09-025-403A-6
US-09-025-403A-6
US-09-025-403A-6
US-09-025-403A-6
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            Sequence
                                                                                                                                                                                                                                                                                                                                                                    Description
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Appli
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US-08-732-708C-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 43, Application US/08732708C Patent No. 6127524
GENERAL INFORMATION:
APPLICANT: Casipit, Clayton L.
APPLICANT: Wong, Hing C.
APPLICANT: Huang, Bee Y.
                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/732,708C
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                               FILING DATE:
ATTORY AGENT INFORMATION:
ANAME: Buchanan, Robert L
REGISTRATION NUMBER: 40,927
REFERENCE/DOCKET NUMBER: 4649
TELECOMPUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: BINDING TITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
            ORIGINAL
                         FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                         TELEX:
                                                                                                                                                                    TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
             SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                          SS: single
linear
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                                                                                                                                          43:
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US-09-025-403A-11
US-09-025-403A-11
US-09-025-403A-11
US-09-025-403A-12
PCT-US94-01709-6
US-08-983-035A-38
US-08-983-081B-8
US-08-232-081B-8
US-08-232-081B-8
US-08-232-081B-3
US-08-871-488A-15
US-08-871-488A-15
US-08-871-488A-19
PCT-US93-00030-2
PCT-US93-00030-2
US-08-822-830B-2
US-08-822-830B-2
US-08-822-830B-1
US-08-822-830B-1
US-08-157-452B-1
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Best Local Similarity
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                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE: 04-DEC-1996
CLASSIFICATION 24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILLING DATE: 05-UN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILLING DATE: 10-CCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILLING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAMES: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELEPHONE: 612/371-5278
TELEPHONE: 612/372-5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
               TOPOLOGY:
                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
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OTHER INFORMATION:
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                                            amino acid
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3100 No. 6111079west
                                                         118 amino acids
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1079west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is Trp,
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Pred. No. 0.0033;
l; Mismatches
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US-08-017-570-6
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                                                                                                                                                                  Query Match
Best Local Similarity
'---hes 9; Conserv:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-767-128-22
                           Sequence 6, Application US/08017570 Patent No. 5472693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Applic
Patent No. 5472693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (517) 636-8104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UNFILING DATE: 19930216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. I
CITY: Midland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       LENGTH:
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AMINO ACID
                                                                                                                                          GFNIKDFYMH 10
                                                                                                                     GFNIKDYYMH 35
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GOURLIE,
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                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOURLIE, BRIAN B
RIXON, MARK W
                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                              94.9%;
BRIAN B
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90.0%;
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                                                                                                                                                                                                Score 56; I
Pred. No. 0.
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Patent No. 5808033
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                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINGEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19930216
CLASSIFICATION: 424
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MEDIUM TYPE: Floppy disk
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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TYPE: AMINO ACID
TOPOLOGY: linear
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STREET: P.O. Box 1967
                                                                                                                                                                 CITY: Midland
                                                                                                                                                                                   STREET:
                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                COUNTRY:
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                                                                                                                 ZIP: 48641-1967
APPLICATION NUMBER:
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MEZES, PETER S
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 US/08/471,426
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Pred. No.
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Best Local 9
                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,570
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT IMPORMATION:
                                                                                        NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: 16-FEB-1993
                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
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TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE:
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CITY: Midland
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                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 06-JU
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9; Conserv
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amino acid
                            amino acid
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                                           124 amino acids
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MEZES, PETER S
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protein
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Best Local Similarity
Watches 9; Conserv:
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SEQ ID NO 1
                                                                                                                                SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Applic Patent No. 6333405
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                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                              PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                            APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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                                                                                                                                                                                                                                                                               APPLICANT:
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TYTLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
                                                                               TYPE: PRT
ORGANISM: Homo sapiens
OTHER IMPORMATION: Amino acid sequence of the human framework regions from OTHER INFORMATION: the NEWM antibody heavy chain variable region, with CDR2 and CDR3
                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
                                      LOCATION: 1..124
                                                 NAME/KEY: Human NEWM VH FR template
                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Murine Col-1 VH
LOCATION: 1..124
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Tempest, Philip R.
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                                                                                                                                                                                                                                                                                          Harris, William J.
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Tempest, Philip R.
Carr, Frank J.
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Pred. No. 0
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Pred. No. 0.0035;
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US-09-672-609-3
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US-09-672-609-2
                                                                                                                                                                                                                                                                                                              US-09-672-609-4
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SOFTWARE: Mi
SEQ ID NO 4
LENGTH: 124
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                             Sequence
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                                                                         FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRICE APPLICATION NUMBER: 09/025,403
                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVH
LOCATION: 1..124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                          4, Application US/09672609
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                                             Microsoft Word 97 SR-2
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Harris, William J.
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Tempest, Philip R.
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Tempest, Philip R.
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                                                                                                                                                            Kathryn
High Affinity Humanized Anti-CEA Monoclonal Antibodies
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Pred. No. 0.0035;
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ORGANISM: Artificial Sequence

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RESULT 12
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US-09-672-609-5
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                                                                                                                                                                                                                      Sequence 6, Application US/09672609 Patent No. 6333405
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Best Local
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Best Local
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 5
        FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
                                                                                             APPLICANT: Harris, William J.

APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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LOCATION: 1..124
COTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
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OTHER INFORMATION:
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NAME/KEY: Humanized COL-1 VH,
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SEQ ID NOS:
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                                                                                                                                                   Tempest, Philip R. Carr, Frank J.
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Pred. No. 0.00
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Pred. No.
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US-09-672-609-7
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PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 7
                                              APPLICANT: Anderson, V
APPLICANT: Tempest, Pl
APPLICANT: Carr, Frani
APPLICANT: Harris, Wi
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Matches
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SEQ ID NO 6
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CURRENT FILING DATE: 2000-09-28
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APPLICANT: Harris, William J.

APPLICANT: Armour, Kathryn

TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
                                  APPLICANT:
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TYPE: PRT
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Humanized COL-1 VH, HuVHAY
LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWN VH FRS, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
OCHER INFORMATION: Ile-29, Lys-30, Tyr-80, Asn-97, and Thr-98
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TYPE: PRT
ORGANISM: Artificial Sequence
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NAME/KEY: Humanized COL-1 VH, HuVHAA
LOCATION: 1..124
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                 TLE OF INVENTION:
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                                                                                    Anderson, W.H. Kerr
Tempest, Philip R.
                                                 Carr, Frank J.
Harris, William J.
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Tempest, Philip R.
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                                Kathryn
               High Affinity Humanized Anti-CEA Monoclonal Antibodies
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Pred. No. 0.0035;
1; Mismatches
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Pred. No. 0.0035;
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Search completed: July 30, 2003, 09:38:27 Job time: 4.22259 secs
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LCCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, Tyr-80, Asn-97, and
OTHER INFORMATION: Thr-98
US-09-672-609-9
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FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHATAY
LOCATION: 1..124
COTHER INFORMATION: Humanized heavy chain variable region containing human
COTHER INFORMATION: NEWM VH FRE, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
COTHER INFORMATION: Ile-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn-97, and Thr-98
US-09-672-609-8
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                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
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SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09672609 Patent No. 6333405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
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CÜRRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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26 GFNIKDYYMH 35
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Similarity 90.0%;
9; Conservative
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                                                                                                                                                                                                           94.9%;
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OM protein - protein search, using sw model
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July 30, 2003, 09:31:34; Search time 5.02658 Seconds (without alignments) 325.245 Million cell updates/sec
                                                                                                                                                                                 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Title: Perfect score: Sequence: US-09-865-198-2 101 1 WIDPENGDSGYAPKFQG 17

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:

283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	" 80	7	6	ហ	4	ω	N		Result No.	
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A;Accession: S25174
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <MON>
A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
A;Accession: S33133
A;Status: preliminary
A;Molecule type: mRNA

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PH1668	C37262	A27646	I44151	S03482	S26911	S31999	PH1666	PH1667	S29594	S24289	S26921	S29544	S26909	S46465	\$49220
	Ċ				Ig heavy chain V r	heavy	_	heavy	_	Ig gamma chain V r		heavy chain	_	_	Ig gamma-1 chain -

ALIGNMENTS

RESULT 2 S25174 Ig heavy chain V region - mouse C;Species: Mus muscullus (house mouse) C;Detc: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000 C;Accession: S25174; S33133 R;Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S. submitted to the EMBL Data Library, July 1992 A;Rescription: Structure and binding properties of monoclonal antibodies to core histone A;Reference number: S25174	Query Match 89.1%; Score 90; DB 2; Length 82; Best Local Similarity 88.2%; Pred. No. 4.6e-07; Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Qy 1 WIDPENGDSGYAPKFQG 17	A;Note: PR8-1 A;Accession: E36025 A;Status: preliminary A;Molecule type: mRNA A;Residues: 19-82 <ca2> A;Cross-references: GB:M57273; NID:g194963; PIDN:AAA38116.1; PID:g194964 A;Note: clone PR8-21 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin</ca2>	n-1991 #sec A36025; E36; A36025; E36; Cad. Sci. L Lad. Sci. L L Lad. Sci. L Lad. Sci. L L Lad. Sci. L L L L L L L L L L L L L L	RESULT 1 A36025 Ig heavy chain V region (PR8-1) - mouse (fragment) C;Species: Mus musculus (house mouse)
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C;Species: Mus musculus (house mouse;
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S15672
C;Accession: S15672
R;Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.;
R;Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.;
Bio/Technology 9, 266-271, 1991
Bio/Technology 9, 266-271, 1991
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A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A;Accession: S15672
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A;Molernle Free Communication of the murine lupus-associated A;Molernle Free Communication of the murine lupus and the murine lupus associated A;Molernle Free Communication of the murine lupus associated A;Molernle Free C
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Eur. J. Immunol. 17, 91-95,
A;Title: Molecular analysis
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S04576
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RESULT
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A; Residues: 1-136 < KOF>
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C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:X58835; NID:g51978; PIDN:CAA41644.1; PID:g51979; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywoxds: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                    79.2%;
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Pred. No. 1.4e-05;
""matches 2;
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Pred. No. 2.5e-05;
0; Mismatches 3
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Pred. No. 1.2e-05;
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A; Nolecule type: DNA
A; Nolecule type: DNA
A; Residues: 1-98 <TOM>
A; Residues: 1-98 <TOM>
A; Cross-references: EMBL: 212317; NID: g32857; PIDN: CAA78187.1; PID 322858
C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                C;Accession: S26918
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winteg
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals a
A;Reference number: S26885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS52445
If heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21_Jan-2000
C;Accession: S52445
                                                                                                                                                                  A; Reference number: A; Accession: S26918
                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Tille: Common structural features among monoclonal antibodies
A;Reference number: A38601; MUID:91115823; PMID:1703527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-115/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-85 < GOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change
C;Accession: E37262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region (6H2) - mouse (fragment) C;Species: Mus musculus (house mouse)
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                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (DP-15) - human (fragment)
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C;Genetics:
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A; Residues: 1-137 <BER>
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75.0%;
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76.5%;
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Pred. No.
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Pred. No. 6.1e-05;
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A;Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
Ig heavy chain precursor V-I region (Nd) - human (fragments) c;Species: Homo sapiens (man) C;Date: 31-Mar-1981 #Bequence_revision 05-Apr-1983 #text_change C;Accession: A93933; A02026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: S31600 R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S31600
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; submitted to the EMBL Data Library, June 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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A; Residues: 1-132 < CUI>
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A; Accession: S31596
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A; Accession: S31600
                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
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Pred. No. 0.0023;
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Pred. No. 0.0031;
                                                                                                                                                                                                                                 Score 67; DB 2;
Pred. No. 0.0032
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                  21-Jan-2000
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                  A; Molecule type: mRNA
A; Residues: 1-110 <HI
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 A;Experimental source:
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.-110 <HIL>

is of germline-encoded VH3 immunoglobulin binding MUID:93301610; PMID:8315388

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staphylc

B cell

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Ig heavy chain V region - human (fragment)
C;Stpecies: Homo sapiens (man)
C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998:
C;Accession: S54912
R;Tomlinson, M.; Walter, G.; Cook, X.Y.Z.; Winter, Gsubmitted to the EMBL Data Library, November 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A; Title: Cloning and sequence determination of the gene A; Reference number: A93933; MUID:83065234; PMID:6815656 A; Accession: A93933
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglol A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-86 <TOMs.
A;Residues: 1-86 <TOMs.
A;Cross-references: EMBL:Z18904; NID:g840779; PIDN:CAA79341.1; PID:g840780
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;3-86/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>
F;30-113/Domain: immunoglobulin homology <IMM>
F;16/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer
F;177-111/Disulfide bonds: #status experimental
                                                                                                                                                    Ig heavy chain V region (clone 2A12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S54912
A; Accession: S54912
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A;Gene: GDB:IGHV@
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A; Contents: annotation; pa:
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A; Residues: 1-143 < KEN>
                                                                                                                               C; Accession: PH1670
                                                                                                                                                                                                                                                        RESULT 12
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Best Local Similarity
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Local Similarity 58.8%;
es 10; Conservation
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Pred. No. 0.0058;
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Pred. No. 0.
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RESULT 15.
$26938
Ig heavy chain V region
C;Species: Homo sapiens
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S23623
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A; Cross-references: EMBL: Z18321
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R; Mariette, X.; Tsapis,
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-171 <OLE>
                                                                                                                                                                                                                                                                                                                                                                                                                      ;Mariette, X.; Tsapis, A.; Brouet, J.C.
ur. J. Immunol. 23, 846-851, 1993
;Title: Nucleotidic sequence analysis of the variable domains of four human monoclonal
;Reference number: 834001; MUID:93209281; PMID:7681398
                                                                                                                                                                                                                                                                   Superfamily: immunoglobulin V region; immunoglobulin homology;Keywords: heterotetramer; immunoglobulin;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                        Accession: S34014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y heavy chain V region - human
;Species: Homo sapiens (man)
;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
;Accession: S34014; S30535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g heavy chain V region precursor - human (fragment)
;Species: Homo sapiens (man)
;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
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Best Local
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Best Local Similarity
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Best Local Similarity
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                                                                                                                 WMNPSSGNTGYAQKFKG
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   (DP-75) - (man)
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52.9%;
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58.8%;
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Pred. No. 0.013;
6; Mismatches
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Pred. No. 0.0076;
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Pred. No. 0.012;
                     human (fragment)
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A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970
A;NOte: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                    문
Search completed: July 30, 2003, 09:44:03 Job time: 5.02658 secs
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A; Residues: 1-98 < TOM>
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Best Local (
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Maximum Match 10
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Perfect score:
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 score greater than or equal
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is derived by analysis of the total
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length:
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RESULT 1 HV1C_HUMAN ID HV1C_HUMAN AC P01744										37 41	36 41		34 41.5	
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HSSP; P01789; IMCP. RGO; G0:0005576; C:extracellular; NAS. RGO; G0:0005576; C:extracellular; NAS. RGO; G0:0003823; F:antigen binding activity; NAS. RGO; G0:0006955; P:immune response; NAS. R InterPro; IPR007110; Ig-like. R InterPro; IPR003106; Ig MHC. DR InterPro; IPR003596; Ig-v. DR Pfam; PF00047; Ig; 1. DR SMART; SM00406; IGv; 1. DR PROSITE; PS50835; IG LIKE; 1. EN PROSITE; PS50835; IG LIKE; 1. EN PROSITE; PS50835; IG LIKE; 1. Query Match Best Local S Matches 10 Immunoglobulin v SIGNAL 1 CHAIN 20 DOMAIN 20 DOMAIN 20 DISÜLFID 41 CONFLICT 21 CONFLICT 53 CONFLICT 125 NON TER 147 SEQUENCE 147 FEQUENCE 147 FEQUENCE 147 FE P01/44; 21-UUL-1986 (Rel. 01, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 15 havy chain V-I region ND precursor (Fragments). Immediate hypersensitivity: modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978). --- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA MEDIINE=83065234; PubMed=6815656; Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney Bell L.O., Gould H.J.; Bell L.O., Gould H.J.; "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982). NCBI_ Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. SEQUENCE FROM N.A. Bennich H.H., Johansson S.G.O., (In) Bach M.K. (eds.); SEQUENCE OF 20-147. SIMILARITY: Contains 1 immunoglobulin-like domain PROTEIN. TaxID=9606; 10; Similarity 1 20 20 20 20 41 41 53 53 53 147 147 Conservative AA; 115 21 54 68 125 16491 58.8%; MW; 4. Score 67; I Pred. No. 0. T -> V (IN REF. 2). IH -> HI (IN REF. 2). VG -> GV (IN REF. 2). MISSING (IN REF. 2). IG HEAVY CHAIN V-I REGION ND IG-LIKE. PYRROLIDONE CARBOXYLIC ACID. 948F9F72A5366C20 CRC64; von Bahr-Lindstrom H.; Mismatches Pyrrolidone carboxylic acid DB 1; .0011; Derbyshire R.B., Viney J., Length 147; Indels 0 Gaps 0

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                                                        01-NOV-1991 (Rel. 20, Created)
01-NOY-1991 (Rel. 20, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-I region V35 precursor.
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21-JUL-1986
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  Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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PIR; A02024; HVHUHG.
HSSP; P01772; 2FB4.
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SMART; SM00406; IGv;
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InterPro; IPR003006; Ig_MHC.
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Rechavi G., Ram D.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983)
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GO:0003823; F:antigen binding activ
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., Glazer L., Zakut

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Pred. No. 0
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                       Craniata; Vertebrata; Euteleostomi;
Catarrhini;
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MEDLINE=21279171; PubMed=11385575; Perraud A.-L., Fleig A., Dunn C.A., Bagley I Schmitz C., Stokes A.J., Zhu Q., Bessman M.J Scharenberg A.M.; Scharenberg A.M.; "ADP-ribose gating of the calcium-permeable "ADP-ribose form of the calcium-permeable Nature 411:595-599(2001).
                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP-ribose pyrophosphatase (EC 3.6.1.13) (ADP-ribose diphosphatase)
ADP-ribose diphosphoribose pyrophosphatase) (ADP-PPase) (ADP-ribose phosphohydrolase) (Nucleoside diphosphate-linked moiety X mogif 9).
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DOMAIN
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MEDLINE=88296408; PubMed=2841108;

Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q:,

Ohno H., Fukuhara S., Honjo T.;

"Dispersed localization of D segments in the human immunoglobulin
                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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SIGNAL 1
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GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heavy-chain locus.";
EMBO J. 7:1047-1051(1988).
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ssman M.J., P
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                                                                                                                                                                                                                                   RESULT 5
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., Male S., Garcia A.M., Gay L.J., Hulyk S.W.,
B RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
B RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
B RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
B RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
B RA Richards S., Worley K.C., Hale S., Sarcia B.J., Lu X., Gibbs R.A.,
B RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
B RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
B Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
B Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew;
MIM; 6
                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- CATALYTIC ACTIVITY: ADP-ribose + H(2)O = AMP +
            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AY026252; AAK07671.1; -. EMBL; BC000542; AAH00542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENÇÉ FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphate.
TISSUE SPECIFICITY: Ubiquitous.
SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. NUDF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , 606022; -.
GO:0005622; C:intracellular; NAS.
GO:0019144; F:ADP-sugar diphosphatase activity; NAS.
GO:0005227; F:calcium activated cation channel activity; NAS.
GO:0006812; P:cation transport; NAS.
                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                             110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00293;
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                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conser
                                                                                                                                                                                                                                                                                         WADPQISESNFSPKF
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350 /
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llarity 46.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUDIX;
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH00542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUDIX;
                                                                                                                                                                                                                                                                                                                                                                                                                                               237
39125
                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                       Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUDIX BOX. ; 2EA5B24B88FB3420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.5
; Mismatches
                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bioinformatics
                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 350;
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Best Local S
Matches 8
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InterPro; 1.
InterPro; 1PR0035-.
InterPro; 1PR0035-.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
SMORY; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKB; 1.
PROSITE; PS50835; IG LIKB; 1.
IG-LIKB:
IG
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P01757;
   DISULFID
NON_TER
SEQUENCE
                                                                                rKUSITE; PS50835; IG LIKE; Immunoglobulin V region.
DOMAIN
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                                                                                                                                                                             SMART:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rearrangements in heavy chain V-region
Nature 283:35-40(1980).
-I- MISCELLANEOUS: THE SEQUENCES OF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55 MEDLINE=83075344; PubMed=6816276;
                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-SEP-2003 (Rel. 42, La
Ig heavy chain V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986
21-JUL-1986
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schilling J., Clevinger B., Davie J.M., Hood L.; "Amino acid sequence of homogeneous antibodies to dextran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=80078170; PubMed=6765983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                    [nterPro; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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                                                                                                                                                                                                                                                                                                                                A26242; MHMSJ5.
; P01789; 1MCP.
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                                                                                                                                                                                                                               IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                               OCCUR IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
22
117
117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01, Last sequence update)
42, Last annotation updat
region J558.
                                                                                                                                                                                                                                                                                                                                                                                                                       THE D AND J SEGMENT
THIS PROTEIN BINDS
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      13024 MW;
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46;
Pred. No.
                                                              IG-LIKE.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEGMENTS
      292E2AF4BE447E41 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHOWN AT 1-7 POSITIONS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene segments.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS
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RESULT 8
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                                                                                                                            P26550;
01-AUG-1992
01-AUG-1992
01-AUG-1992
                SEQUENCE FROM N.A.
MEDLINE=13106467; PubMed=1649510;
MEDLINE=1306467., Fitsumoto T., Ka
Yabe Y., Sakai A., Hitsumoto T., Ka
"A subtype of human papillomavirus
segment amplified in a carcinoma: n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.

MEDLINE=84182519; PubMed=6201362;

NITHON R. BOVENB J., Siekevitz M.,
organizations.";
Virology 183:793-798(1991)
                                                                                              Probable E4 protein.
Human papillomavirus type 5b.
Viruses; dsDNA viruses, no RNA
                                                                                                                                                                                                                                                                                                        DISULFID NON_TER
                                                                           NCBI_TaxID=10599;
                                                                                                                  Probable E4
                                                                                                                                                                                                                                                                                               SEQUENCE
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EMBO J. 3:5:
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15-JUL-1999
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                                                                                      Papillomavirus.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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PS50835; IG LIKE;
obulin V region.
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9 (Rel. 38, Last ann
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06, Last sequence update)
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Pred. No.
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J SEGMENT.
BY SIMILARITY.
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                Kato H., Ogura H.;
is 5 (HPV-5b) and its subgenomic
nucleotide sequences and genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed
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01-NOV-1997
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum (Wheat).
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae; Pooideae;
 EMBL; X12928; CAA31395.1;
InterPro; IPR001419; Glute
Pfam; PF03157; Glutenin_hr
                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                        SUBMITTED (FEB-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED PROTEIN OF WHEAT ENDOSPERM. THOUGHT OBE RESPONSIBLE VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.

-!- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
-!- MISCELLANEOUS; GLUTENINS ARE CODED BY SEVERAL GENES ON GROUP 1 CHROMOSOMES OF WHEAT.
-!- MISCELLANEOUS; THE MATURE PROTEIN IS CHARACTERIZED BY NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLT5_WHI
P10388;
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                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Cheyenne;
MEDLINE=89098419; PubMed=2563152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glutenin, high molecula GLU-1D-1D OR GLU-D1-1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHEAT
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                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                         REVISIONS,
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                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 17:461-462(1989).
                                                                                                                                                                                                                                                                                                                                         "Nucleotide sequences of the two high-molecular-weight from the D-genome of a hexaploid bread wheat, Triticum
                                                                                                                                                                                                                                                                                                                                                                  Malpica-Romero J.M.;
                                                                                                                                                                                                                                                                                                                                                                            Anderson O.D.,
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igh molecular weight subunit DX5 p
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Glutenin_hmw;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG_LIKE; 1.
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                                                                                                                                                       CHAIN
DOMAIN
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"Developmentally controlled and tissue-specific expression unrearranged VH gene segments.";
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Mammalia; Eutheria;
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Mus musculus (Mouse)
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Seed storage protein;
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DOMAIN
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HSSP; P01810; 2FBJ.
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                                                                                                                                                                                                                                                                                                                entities requires a license agreement
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in V region VH558 Al/A4 precursor.
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Pred. No.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
                                                                                                                                          IG HEAVY CHAIN V REGION VH558 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLUTENIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene family; Signal
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                                                                               8B0BC138856DFC9D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                        Mismatches
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                 REGION VH558 A1/A4.
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                                                         Length 117;
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VEALURY 11

VEALURY 15

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RESULT 12
GLT1_WHEAT
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Best Local
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P06924;
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P02861;
                                                                                                                        SEQUENCE FROM N.A.

FORDE J., FORDE B.G., Fry R.P., Kreis M., Shewry P.R., Mifl Forde J., Forde B.G., Fry R.P., Kreis M., Shewry P.R., Mifl "Identification of barley and wheat cDNA clones related to M-r polypeptides of wheat gluten.";
FEBS Lett. 162:360-366(1983).
-I- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE F VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
-I- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
-I- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON GROUP 1 CHROMOSOMES OF WHEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type 5.";
Virology 158:251-254(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-UTL-1986 (Rel. 01, Created)
21-UTL-1986 (Rel. 01, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
Glutenin, high molecular weight subunit PC256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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01-FEB-1996
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M17463; AAA46987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87207670; PubMed=3033892; Zachow K.R., Ostrow R.S., Faras A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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NCBI_TaxID=10578;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum (Wheat)
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"Nucleotide sequence and genome organization
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DNA viruses, no RNA
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33, Last sequence update)
33, Last annotation update)
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61.5%;
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Pred. No. 6.
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RESULT 13
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Matches 6
              EMBL; L10631; -; NOT ANNOTATED_CDS.
HSSP; P06201; 1LGR.
InterPro; IPR001691; GLN synth.
InterPro; IPR004809; GlnA.
InterPro; IPR001637; GlnA adenyltn.
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    Pfam;
Pfam;
                                                                                                                                   the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. I
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                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93273742; PubMed=8099074;
Hosted T.J., Rochefort D.A., Benson D.R.;
"Close linkage of genes encoding glutamine synthetases I Frankia alni CpI1.";
J. Bacteriol. 175:3679-3684(1993).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last amotation update)
Glutamine synthetase I (EC 6.3.1.2) (Glutamate--ammonia ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Bacteria; Actinobacteria;
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                                                                                                                                                                                                                                             HEXAGONS.
SUBCELLULAR LOCATION: Cytoplasmic.
SUSCELLANEOUS: TWO FORMS OF GLUTAMINE SYNTHETASE (CAN BE FOUND IN THIS NITROGEN FIXING BACTERIA, GSI
CAN BE FOUND IN THIS SYNTHETASE WHEREAS GSII IS SI
                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                  SUBUNIT: OLIGOMER OF 12 SUBUNITS
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S; PR00210; GLUTENIN.
PF00120; gln-synt; T
PF03951; gln-synt_N;
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Pred. No. 3.4;
1; Mismatches
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RESULT 15
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PROSITE; P
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                                                                                                                                                                                                                                                                                                                                                                                  George A.M., Hall R.M., Stokes H.W.;
"Multidrug resistance in Klebsiella pneumoni
confers a multidrug resistance phenotype in
Microbiology 14:1909-1920(1995).
-!- SIMILARITY: TO M.TUBERCULOSIS RV0906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROMA_KLEPN STANDARD; PRT; 132 AA (948412)
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nitrogen fixation; Ligase; Multigene family.
BINDING 402 402 AMP (UNDER CONDITIONS OF ABUNDANT GLUPANINE) (BY SIMILARITY).
SEQUENCE 474 AA; 53951 MW; FEIDB19AC1735652 CRC64;
                                                                                                                                                                                                                                                    EMBL; U19581; AAA85696.1; PIR; T09626; T09626.
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PS00181; GLNA_ATP; 1.
PS00182; GLNA_ADENYLATION; 1.
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Pred. No. 6.6;
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19;
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P16624; 01-AUG-1990 (Re 01-AUG-1991 (Re 01-OCT-2001 (Re 17 kDa surface

(Rel. (Rel. (Rel.

15, Created)19, Last sequence update)40, Last annotation update)

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Search completed: July 30, 2003, 09:44:59 Job time: 3.65449 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-Madrid E;
MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=Madrid E;

MEDILINE=89359171; PubMed=2768201;

Anderson B.E., Tzianabos T.;

"Comparative sequence analysis of a genus-common rickettsial antigen gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OMP OR RP833.
Rickettsia prowazekii.
Rickettsia, Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                              PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.
SIGNAL 1 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 396:133-140(1998).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 171:5199-5201(1989).
                                                                102 WRNPDNGNHGY 112
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20
159 AA;
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20 N-ACYL DIGLYCERIDE (PROBA
16672 MW; A33D404B65EEB071 CRC64;
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SUMMARIES

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Q99L31;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
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Q96GA6
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 468 AA; 51661 MW;
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HSSP; P01842; 7FAB.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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PRELIMINARY;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003306; Ig_W.
InterPro; IPR003396; Ig_V.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGV; 1.
PROSITE; PS00041; HTH ARAC_FAMILY_1; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_MHC; 3.
HYDOTHER (3-1 NOTHER)
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InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
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01-DEC-2001
01-DEC-2001
01-MAR-2003
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
Anti-myosin immunoglobulin h
                                                                                                                                                                                                                                                                                                                                                                                                              Infect. Immun. 68:5803-5808(2000)
EMBL; AF206021; AAF69319.1; -.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20448942; PubMed=10992488; Malkiel S., Liao L., Cunningham M.W., Diamond B.; "T-Cell-dependent antibody response to the dominant streptococcal polysaccharide, N-acetyl-glucosamine,
                                                                                                                                   SEQUENCE
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Mammalia; Eutheria; Rodentia;
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SEQUENCE 6
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Submitted (JUL-2001) to the
EMBL; BC009851; AAH09851.1;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with cardiac myosin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9JL85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=B-cell;
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[1]
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11; Conserv
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                                                                                                                                11944 MW; DFE615FE6CED4EDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.4%;
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heavy chain variable region
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                             Score 57; DB 1
Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58; DB Pred. No. 1.1;
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Sciurognathi; Muridae;
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01-MAR-2002
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                 Pfam;
                                                                                                                                 down-regulated in colorectal submitted (JUN-2000) to the EMBL; AF283666; AAL36987.1;
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Mammalia; Eutheria;
                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 4.
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EMBL; AJ224083; CAA11829.1;
HSSP; P01772; 2FB4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                   Zheng S., Shao X., Cao J., Geng L., I "Identification and characterization
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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SMART; SM00406; IGv;
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Catarrhini;
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                                                                                                                                                                                                                      g Y., Dong Q.;
SNC66, a Ig-like
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Best Local S
Matches 9
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PKELLINI

Q9UL94;

Q1-MAY-2000 (TrEMBLrel. 13, Created)

Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)

Q1-MAR-2003 (Tremblinel. 23, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 497 AA; 53665 MW;
                                                                                                                                                       .NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UL95
   SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                                                                           Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol.
EMBL; AF035019; AAD56255.1;
HSSP; P01810; 2FBJ.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Pred. No.
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                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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OBVCV5; CTEMBLrel. 20, Cree
O1-MAR-2002 (TrEMBLrel. 20, Last
O1-MAR-2003 (TrEMBLrel. 23, Last
O1-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical 52,3 kDa protein.
Mus musculus (Mouse)
                                                                                           Q9UL92;
Q9UL92;
Q1-MAY-2000
01-MAY-2000
01-MAR-2003
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Clin. Immunol. Immunopathol. 87.
EMBL; AF035020; AAD56256.1; -.
HSSP; P01810; 2FBJ.
Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SMART; SM00406; IG:
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                               Myosin-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
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9; Conserv
                                                                                                                                                                                                                                                                                                     WIDPENGDSGYAPKFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WINPNSWTTNYAQKFQG
                                                                                                                                                                                                                                                                             YIDPYNGGSSYNQKFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WIDPENGDSGYAPKFOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AA;
                                                                                               (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGv; 1.
35; IG_LIKE;
                                                                         EMBLrel. 13, Last sequence update)
EMBLrel. 23, Last annotation updat
immunoglobulin heavy chain variab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13205 MW;
  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.5%;
                                                                                                                                                                                                                                                                                                                                                                        53.5%;
                                                                                               13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            س
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54;
Pred. No.
                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87:184-192 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
    Craniata; Vi
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                      52B44C5826807143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in rheumatic carditis
                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
                                                                                                                                                                                                                                                                                                                                                                            54;
No.
                                                                                                                                                                               124
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                    Vertebrata;
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    Hominidae;
                                                                               on update)
1 variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Length
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                        Euteleostomi;
                                                                               region
      ното
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                                                                                                                                                                                                                                                                                                                                                                                                 481;
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RESULT 11
Q8NCB9
ID Q8NCB9
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                                                                                                                                                                                                     Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                         SMART; SM00409; ĬĠ; 3.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00299; IG_MHC; 2.
SEQUENCE 480 AA; 51645 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBK0Z4;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to expressed sequence AI893585.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2002) to the EMBL; BC029188; AAH29188.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8K0Z4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu X., Liu B., Van der Merwe P.L., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TER
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                                                                                               - S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
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                                                                                                                                                                                                     Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity Gonserva
                                                                                                               WISPGDGSSEYNEKFKG
                                                                                                                                                         WIDPENGDSGYAPKFQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124
124 AA;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124
; 13580 MW;
                                                                                                                                                                                                                          50.5%;
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Pred. No. 2.3;
2; Mismatches
                                                                                                                                                                                                                          Score 51;
Pred. No.
PRT;
                                                                                                                                                                                                                                                                                           8690A63C669CDBED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalis N.N.,
300
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2.3;
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                                                                                                                                                                                                                                             Length 480,
                                                                                                                                                                                                     Indels
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RESULT 12
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Best Local :
                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                              Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027295; BAB55021.1; -
InterPro; IPR000086; NUDIX hydrolase.
Pfam; PF00293; NUDIX; 1.
Hypothetical protein.
SEQUENCE 350 AA.
                                                                                                                                                                                              TISSUE-Embryo;
IISSUE-Embryo;
IISOgai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki I., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Masahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi @Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saigo K., Watanabe S., Kimura K., Marakamura Y., Nagahari K., Masuho Y.,
                                                                                                                                                                                                                                                                                                                                                                                            Q96KB3;
Q96KB3;
01-DEC-2001
01-DEC-2001
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8NCB9;
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "NEDO human CDNA sequencing project.";
"NEDO human CDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK074845; BAC11239.1;
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein FLJ14389.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000086; NUDIX hydrolase. Pfam; PF00293; NUDIX; 1.

Hypothetical protein.
SEQUENCE 300 AA; 33776 MW; 531993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                       1 WIDPENGDSGYAPKF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WIDPENGDSGYAPKF
                                                  Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WADPQISESNFSPKF
                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 19, Creat
(TrEMBLrel. 19, Last
(TrEMBLrel. 22, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence up)
(TrEMBLrel. 23, Last annotation)
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleos
Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primates;
                                                                49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.5%;
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                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531993C757A82E49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                   Mismatches
                                                                           50;
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RESULT 13

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Q8NBN1;

PRELIMINARY;

PRT;

350 AA.

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QBKLJA
QBKLJA
AC QBKLJ
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DT 01-QC
DT 01-MA
DE Simil
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DE SIMIL
DE GUARA
OC EUKAZ
OC MAMMA
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RN [1]
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ACCOR
RESULT
Q8BVU5
ID Q8
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DT 01
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Best Local S
Matches 7
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Best Local Similarity
Matches 7; Conserv
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01-MAR-2003 (TrEMBLrel. 22, Last sequence update)
Hypothetical protein NT2RP2002907.
Homo sapiens (Human).
Eukaryota; Metarr
                                             Q8BVU5;
Q8BVU5;
01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ |
EMBL; BC033921; AAH33921.1; -.
InterPro; IPR000086; NUDIX_hydrolase.
Pfam; PF00293; NUDIX; 1.
Pfam; PF00293; NUDIX; 1.
SROUENCE 350 AA; 38623 MW; 6FD9371307AB336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8K1J4
Q8K1J4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Nagahari K., Sugano S., Isogai T.;
"HRI human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK075408; BAC11601.1;
InterPro; IPR000086; NUDIX hydrolase.
Pfam; PP00239; NUDIX; 1.
Hypothetical protein.
SEQUENCE 350 AA; 39095 MW; 2EB6A14B9BE83420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to nudix (Nucleoside diphosphate linked moiety X)-type motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y.,
Vamamoto J., Wakamatsu A., Nagai T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
  Mus musculus (Mouse).
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                                                (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Primates;
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Rodentia;
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Pred. No. 11;
4; Mismatches
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Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6FD9371307AB3366 CRC64;
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Nakamura Y.,
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                                                Query Match
Best Local S
Matches 7
                                                                                                the RIKEN Genome Exploration Research Group ("Analysis of the mouse transcriptome based 0",770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK076500; BAC36366.1; -
SEQUENCE 350 AA; 38604 MW; EDD9371307AB
                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
STRAIN=S154683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
 110
                         1 WIDPENGDSGYAPKF 15
                                                Similarity 7; Conserv
WADPQISESNFSPKF
                                                  Conservative
                                                            49.5%; Score 50; DB 46.7%; Pred. No. 11;
 124
                                                  4;
                                                                                                 EDD9371307AB3373 CRC64;
                                                  Mismatches
                                                                                                                                                                  Group
                                                                        11;
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Job time Search completed: July 30, 16.2706 secs 2003, 09:42:32 THIS PAGE BLANK (USPTO)

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Result
No.
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Perfect score:
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

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158.727 Million cell updates/sec
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(c) 1993 - 2003 Compugen Ltd
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ABJ26719
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                                                                                   Complementary dete
Mouse anti-KDR plC
Heavy chain comple
VEGF binding relat
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Mouse anti-KDR plC
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Antigen-binding pr
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23	20	20	20	20	20	20	20	20	20	20	15	15	20	21	20	21	20	24	23	23	23	23	22	22	23	24	23	22	22	24	23	22	22	24	23
ABB83941	AAY39543	AAY39542	AAY39541	AAY39540	AAY39539	AAY39538	AAY39537	AAY39536	AAY39530	AAY39528	AAR60566	AAR60565	AAY39531	AAY70787	AAW89173	AAY70794	AAW89162	ABJ26732	AAU74420	AAE25963	AAE25961	AAE28916	AAB82701	AAE13145	AAE25965	ABJ26729	AAU74417	AAB82709	AAE13143	ABJ26728	AAU74416	AAB82704	AAE13138	ABJ26731	AAU74419
Mouse monoclonal a	Humanised Murine C	Murine	Murine	Murine	Humanised Murine C	Humanised Murine C	Humanised Murine C	Murine	Murine	Murine COL1 VH cha	Anti-carcinoembryo	Anti-carcinoembryo	Humanised Murine C	Murine anti-p53 mo	Anti-p53 monoclona	Murine anti-p53 PA	Anti-p53 monoclona	VEGF binding relat	₽		KDR binding immuno	11 vector	VEGF antagonist an	Chimeric p1C11 hea			en-binding	VEGF antagonist an	Humanised antibody	VEGF binding relat		VEGF antagonist an	П	\mathbf{L}	Antigen-binding pr

ALIGNMENTS

RESULT 1 AAY97230

AAY97230;

AAY97230 standard; Protein; 17

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glioblastoma multiforme; hemangioblastoma; AIDS; central nervous system neoplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human. 29-JAN-1999; 29-JAN-1999; Synthetic Immunoglobulin; antibody; complementary determing region; CDR; VEGF; vascular endothelial growth factor; KDR; versular endothelial growth factor; KDR; kinase insert domain contening receptor; multivalent; monovalent; kinase insert domain contening receptor; multivalent; triabody; humanised antibody; chimeric antibody; tumour; diabody; triabody; Complementary determining region (CDRH2) of anti-SI(KDR) antibody 19-DEC-2000 (IMCL-) IMCLONE SYSTEMS INC 28-JAN-2000; 03-AUG-2000 WO200044777-A1 Homo sapiens. (first entry) 2000WO-US02180 99US-0117726. 99US-0240736.

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RESULT 2
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                                                                                                                               WPI; 2002-589175/63.
N-PSDB; AAD42815.
Novel immunoglobulin molecule for reducing tumor kinase insert domain-containing receptor with an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR; foetal liver kinase; FCK-1 receptor; vascular endothelial growth facto VEGF; tumour growth; heavy chain complementarity determining region 2; CDRH2; angiogenesis; plCl1; scFv antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise
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            The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting VEGF induced reducing endothelial cell proliferation; inhibiting VEGF induced
                                                                                                                                                                                             New bispecific immunoglobulin-like antigen-binding protein tumour growth and for inhibiting angiogenesis, comprises a two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel immunoglobulin molecule that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR plC11 scEV antibody heavy chain complementarity determining region 2 (CDRH2).
                                                                                                                                                                  Claim 55; Page 56; 64pp; English.
                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                           WPI; 2002-106189/14.
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                          The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse peptide relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; antibody; antigen binding site; VEGF receptor; leukaemia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; mouse; murine.
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Pred. No. 1e-08;
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                                                                extracellular domain of the KDR receptor with the same affinity VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have
                                                                                                                                          New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a triabody, a humanised antibody or a chimerised antibody. The immunoglobulin molecules bind specifically to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGF; vascular endothelial growth factor; KDR; kinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody;
                                        applications in treating these conditions. preferred heavy chain complementary determine
                                                                                                                                                                                                                                                                Claim 4; Page
                                                                                                                                                                                                                                                                                          Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor, used to reduce tumour growth
                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-1999;
29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         central nervous system neoplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glioblastoma multiforme; hemangioblastoma; AIDS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variable heavy chain fragment of anti-SI(KDR) antibody.
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                        mmunoglobulins of the invention.
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117 AA;
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99US-0240736.
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                                         determining
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Query Match

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Matches 17
                                                                                                                                                                                                                                The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FIK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR plCl1 scFv antibody heavy chain variable region (VH).
  AAU74412;
                            AAU74412 standard; peptide; 117
                                                                                                                                                                                                                                                                                                                                                                                               Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable kinase insert domain-containing receptor, and neutralizes activation human vascular endothelial growth factor, and neutralizes activation
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N-PSDB; AAD42820.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; immunoglobulin; kinase insert domain-containing receptor; KD foetal liver kinase; FLK-1 receptor; vascular endothelial growth fa VEGF, teumour growth; heavy chain variable region; VH; anglogenesis; Pleck Sefv antibody.
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 11; 34pp; English
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(WITT/) WITTE L.
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factor;
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                                                                                  Matches
                                                                                                                                                                                                                      and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (1) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an 1gG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain (VH) incorporated into Fv, an engineered protein containing a heavy chain variable domain described in
                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor, reducing tumour growth; inhibiting angiogenesis, reducing endothelial cell proliferation; inhibiting VEGF induced reducing endothelial cell proliferation; inhibiting VEGF induced migration of human leukaemia cells; blocking interaction of approtein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 57; Page 57; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen-binding protein; cytostatic; angiogenesis vascular endothelial grow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS20283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhu Z;
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17; Conserv
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                                                                                                   100.0%;
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                                                                                                   Score 101; DB 23;
Pred. No. 7.9e-08;
                                                                              Mismatches
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                     VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
                                                                                                                                                                                                    AAE25960 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7;
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US2002064528-A1
                          Mus sp
                                                               Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR; foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor; VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;
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                                                     antibody
                                                                                                                    immunoglobulin related mouse protein
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-301299P
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002WO-US20332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         related protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49; 98pp;
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A
                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                      66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID
                                                                                                                                                                                                                                                                                                                       Score 101; DB 24;
Pred. No. 7.9e-08;
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                                                                                                                    #1.
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                                                                                                                                                                                                                                                                                                                                                    117;
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ARBSULT 10
AAU74419
ID AAU74
XX AATig
AX AAtig
AX AAtig
KW Cytose
KW Cytose
KW Cell
XX Cell
XX Synth
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Matches
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VBGP) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is KDR binding immunoglobulin related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhu
                                                                                                                                                                                                                     Antigen-binding protein; single chain variable fragment; cytostatic; angiogenesis inhibitor; tumour; leukaemia; an vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                         Region
                                                                                         Region
                                                                                                                                                                                  Mus sp.
Synthetic
                                                                                                                                                                                                                                                                                      Antigen-binding protein, single chain variable fragment version
                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                     AAU74419 standard; Protein; 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (/ITIM)
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                                                                                                                                            Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-589175/63.
DB; AAD42824.
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17; Conser
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WITTE L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIDPENGDSGYAPKFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                     WIDPENGDSGYAPKFOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to novel immunoglobulin molecules that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 16-17; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001US-0976787.
                                                                                                                                                                                                                                                                                                                   (first entry)
                           133..240
 /note= "Light chain variable domain. Specifically
                                                                 /note=
                                                                                                    /note= "Heavy chain variable domain.
claimed in claim 57"
                                                                                                                               /label= VH
                                                                                                                                                        Location/Qualifiers
              /label=
                                    "15 amino acid linker joins the VH and regions of the single chain variable fragment protein. Encoded by AAS20285'
                2
                                                                              Linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 1.7e-07;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                        AAS20285"
                                                                                                                   Specifically
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                                                                                                                                                                                                                                                               scFv;
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                                                                                                                                                                                                                                                              antigen;
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RESULT 11
ABJ26731
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 17
                                               Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis; leukaémia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; mouse: murine.
               Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides -
                                                                                                                         VEGF binding
                                                                                                                                                             01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                    ABJ26731 standard; Protein; 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 63; Page 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-106189/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2000; 2000US-206749P.
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                                                                                                                                                                                                                                                                                                                             50
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17; Conserv
                                                                                                                                                                                                                                                                                                                           WIDPENGDSGYAPKFQG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 AA
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                         related
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                         protein
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                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101; DB 23;
Pred. No. 1.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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RESULT 12
AAE13138
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (WEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
                       Witte L,
                                                                                                                                                                                                                                                                                                                                                                                                   Mus
                                                                                (IMCL-)
                                                                                                                                                                      31-MAR-2000;
                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US10504.
                                                                                                                                                                                                                                                                                                                                             WO200174296-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocytic;
Hodgkin's di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vascular endothelial growth factor receptor; VEGFR; antagoni cytostatic; heavy chain hypervariable region; VH; myelocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised antibody murine heavy chain hypervariable region (VH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE13138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New bispecific antibodies having antigen-binding sites specific for first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells, or for treating tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2002; 2002WO-US20332
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                                                                                IMCLONE SYSTEMS INC. CORNELL RES FOUND IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIDPENGDSGYAPKFQG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIDPENGDSGYAPKFOG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erythrocytic; monocytic;
                                                                                                                                                                      2000US-0540770.
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Pred. No. 1.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ic; multiple myeloma; lympl
determining region-2; CDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                cumour,
leukaemia;
mphoid cell
'R-2;
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Best Local
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Treating or controlling an angiogenic dependent condition (e.g. a
                                 WPI; 2001-514531/56
                                                                                                                                          28-JAN-2000;
31-MAR-2000;
                                                                                                                                                                                        29-JAN-2001; 2001WO-US02839
                                                                                                                                                                                                                                                       WO200154723-A1
                                                                                                                                                                                                                                                                                     Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                  Chimeric
                                                                                                                                                                                                                                                                                                                                     complementarity determining region
                                                                                                                                                                                                                                                                                                                                                  colon carcinoma; ovarian carcinoma;
glioblastoma multiforme; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                           IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
vascular endothelial growth factor; angiogenesis; antiangiogenic;
antitumour; neoplasm; collagen-vascular disease; autoimmune disea
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEGF antagonist antibody IMC-1C11 VH CDR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB82704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB82704 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanis antibody murine heavy chain hypervariable region (VH) CDR-2 used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth factor receptor (VEGFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 14; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-662942/76.
N-PSDB; AAD21664.
                                                                                                                                                                                                                                                                                                                                                                                   tumour; breast carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour cells that are stimulated by a ligand of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rowth factor receptor (VEGFR) in mammals particularly humans. The method nvolves treating the mammals with humanised VEGFR monoclonal antibodies
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                                                                                              SUNNYBROOK HEALTH SCI CENT. IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIDPENGDSDYAPKFQG 17
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                                                                                                                                                                                                                                                                                                    Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AA;
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                                                                                                                                          2000US-0178791.
2000US-0539692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.1%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to a method for inhibiting the growth of non-solid stimulated by a ligand of vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                 lung carcinoma; prostate carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94;
                                                                                                                                                                                                                                                                                                                                                  therapy; heavy chain; CDR
                                                                                                                                                                                                                                                                                                                                                                  neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is humanised (VH) CDR-2 used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used in the
                                                                                                                                                                                                                                                                                                                                                                                                  disease;
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-IC11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma system tumour, ovarian carcinoma, neuroblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endothelial growth factor (VEGF) antagonist activity. The antibor of a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce anti-angiogenic molecule and a chemotherapeutic agent, to produce
New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                    Complementarity determining region; CDR; CDRH2; antigen; cytostatic; angiogenesis inhibitor; vascular endothelial growth factor receptor; VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU74416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU74416 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 of the heavy chain variable region (see also AAB82701) of
IMC-1C11, a mouse-human chimeric antibody that has vascular
endothelial growth factor (VEGF) antagonist activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 37; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neoplasm, collagen-vascular or autoimmune disease) in mammal k
                                                                                  WPI; 2002-106189/14
                                                                                                                                                                                    24-MAY-2000; 2000US-206749P.
                                                                                                                                                                                                                    24-MAY-2001; 2001WO-US16924.
                                                                                                                                                                                                                                                       29-NOV-2001
                                                                                                                                                                                                                                                                                         WO200190192-A2
                                                                                                                                                                                                                                                                                                                                                        antibody
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                                                                    AAS20287.
                                                                                                                                                     IMCLONE SYSTEMS INC
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                                                                                                                                                                                                                                                                                                                                                          heavy chain variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          determining region
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Pred. No. 1.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (CDRH2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
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Best Local S
Matches 16
                              New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; mouse; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                        WPI; 2003-201468/19
                                                                                                                                                                                                                                    26-JUN-2001; 2001US-301299P
                                                                                                                                                                                                                                                                       26-JUN-2002; 2002WO-US20332
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                                                                                                                                                                                                                                                                                                                                             WO2003002144-A1
                                                                                                                                                                                                                                                                                                                                                                               ds snw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGF binding related peptide SEQ ID No 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABJ26728;
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                                                                                                                                                                                                (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABJ26728 standard; Peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WIDPENGDSGYAPKFOG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIDPENGDSDYAPKFQG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 60; 64pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         describes an antigen-binding protein (I) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ß,
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Pred. No. 1.2e-07;
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Claim 10; Page 53; 98pp; English

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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                  The invention relates to a novel antibody having a first antign binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse peptide relating to the invention.
                                                                                                                                                  Sequence
                                    1 WIDPENGDSGYAPKFQG 17
WIDPENGDSDYAPKFOG
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                                                                          Conservative
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                                                                                            Score 94; DB 24; Length 17; Pred. No. 1.2e-07;
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Search completed: July 30, 2003, 09:36:45 Job time : 18 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

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9 US-09-976-787-22
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10 US-09-976-787-23
10 US-09-976-787-23
11 US-09-9786-198-22
11 US-09-976-787-29
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     US-09-865-198-28
US-09-798-689-21
US-10-032-482-18
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Sequence 2, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 28, Appl
Sequence 28, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 27, Appl
Sequence 27, Appl
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US-09-976-787-2
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LENGTH: 17
TYPE: PRT
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Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR PILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 66/117,726
PRIOR RILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
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equence 8, Appl	equence 7, Appl	quence 6,	equence 5, Appl	equence 4, Appl	equence 3, Appl	equence 1,	equence 12, App	equence 11,	equence 10,	equence 9, Appl	equence 8, Appl	equence 7, Appl	equence 6, Appl	equence 5,	equence 4, Appl	equence 3, Appl	equence 1, Appl	equence 12, App	e 11,	equence 10,	equence 9,	equence 8, Appl	equence 7, Appl	equence 6, Appl	е 5,	equence 4, Appl	equence 3, Appl	equence 1,	equence 7,

ALIGNMENTS

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RESULT 2
US-09-865-198-2
; Sequence 2, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
                                                                                                                                                                                                                         ; ORGANISM: Mus musculus US-09-976-787-2
                                                                                                                                                                 1 WIDPENGDSGYAPKFQG 17
                                                                                                             WIDPENGDSGYAPKFOG
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; CRGANISM: Mouse
US-09-865-198-2
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Patent No. US20020103345A1
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Best Local (
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SEQ ID NO 2
LENGTH: 17
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                                    FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR AMPLICATION NUMBER: US 60/206,749
PRIOR PILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
SOPTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                      APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
TITLE OF INVENTION: Production
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CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
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CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
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TITLE OF INVENTION: Antibodies Specific to
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; ORGANISM: Mouse US-09-865-198-27
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US-09-865-198-7
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US-09-976-787-28
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Best Local Similarity
Matches 17; Conserv
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                                                                      Query Match
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PRIOR FILING DATE: 2000-05-24
NUMBER OF THE PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                           TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and MethorITITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Antibodies Specific to FILE REFERENCE: 11245/46505
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                                                                                                                                            LENGTH: 240
TYPE: PRT
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                                   Local Similarity hes 17; Conserv
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WIDPENGDSGYAPKFQG 17
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Conservative 0
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                                                     Score 101; DB 10;
Pred. No. 5.1e-08;
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Pred. No. 5.1e-08;
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Pred. No. 2.4e-08;
                                       Mismatches
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RESULT 9
US-09-976-787-23
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SOFTWARE: WordPerfect 8.0
SEQ ID NO 21
LENGTH: 17
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Patent No. US20020103345A1
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LENGTH: 17
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Patent No.
                                                                                                                      Sequence 23, Application US/09976787 Patent No. US20020064528A1
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Best Local Similarity
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APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
TITLE REFERENCE: 11245/46505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methotitics of INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR PILING DATE: 2000-05-24
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-09-976-787-22
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CURRENT FILING DATE: 2001-10-12
PRIOR PPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
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TITLE OF INVENTION: Antibodies Specific to KDR
FILE REFERENCE: 11245/46505
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APPLICANT: Witte, Larry
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o. US20020064528A1
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Pred. No.
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Pred. No.
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; ORGANISM: Mouse
US-09-865-198-22
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US-09-865-198-22
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APPLICANT: Zhu, Zhenping
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methoritite OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT APPLICATION NUMBER: US/09/865,198
PRIOR APPLICATION NUMBER: US/09/865,749
PRIOR APPLICATION NUMBER: US/09/86/749
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                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09798689 Publication No. US20030103973A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                               APPLICANT: Goldstein, Neil I.

TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/401,163
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 08/67,113
PRIOR FILING DATE: 1997-011-10
PRIOR PILING DATE: 1997-011-10
PRIOR FILING DATE: 1997-011-10
PRIOR FILING DATE: 1998-09-03
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CURRENT FILLING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                  APPLICANT: Rockwell, Patricia APPLICANT: Goldstein, Neil I.
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TYPE: PRT
                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
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1995-06-07
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94.1%;
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94.1%;
                  08/476,533
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Pred. No. 2.9e-07;
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Pred. No. 2.9e-07;
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; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29
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; ORGANISM: Mouse US-09-865-198-28
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US-09-865-198-28
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                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
                                                    SOFTWARE: WordPerfect
SEQ ID NO 28
LENGTH: 238
                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/09865198 Patent No. US20020103345A1
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Best Local :
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APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
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TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CÜRRENT APPLICATION NUMBER: US/09/976,787
CÜRRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
                                                                                                                              CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                  NUMBER OF SEQ ID NOS:
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ORGANISM: Mouse
                                      TYPE: PRT
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Pred. No. 6.1e-07;
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Pred. No. 2.9e-07;
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US-09-798-689-21
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CURRENT APPLICATION NUMBER: US/10/032,482
CURRENT FILING DATE: 2002-01-02
PRIOR APPLICATION NUMBER: US/09/445,602
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: PCT/IL98/00266
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: IL 121041
PRIOR APPLICATION NUMBER: IL 121041
PRIOR PILING DATE: 1997-06-09
                                                                                                                                                                                                                                                          Sequence 18, Application US/10032482
Publication No. US20020197270A1
GENERAL INFORMATION:
APPLICANT: Cohen, Irun
APPLICANT: ROTTER, Varda
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PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 08/90
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 08/70
PRIOR FILING DATE: 1996-09-03
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Best Local Similarity
Matches 16; Conser
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                                                                                                                                        APPLICANT: HERKEL, Johannes
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNITY
FILE REFERENCE: COHEN42
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PRIOR FILING DATE: 1995-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1994-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Method for Reducing Tumor Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                          Wolkowicz, Roland
RUIZ, Pedro
EREZ-ALON, Neta
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No. US20030103973A1
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Goldstein, Neil I.
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94.1%;
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Pred. No. 6.1:
0; Mismatches
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6.1e-07;
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; NUMBER OP.SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
ORGANISM: Mus musculus
US-10-032-482-18
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1 WIDPENGDSGYAPKFQG 17

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Search completed: July 30, 2003, 10:20:28 Job time: 20.897 secs

Query Match 89.1%; Score 90; DB 14; Length 17; Best Local Similarity 88.2%; Pred. No. 1.6e-07; Matches 15; Conservative 1; Mismatches 1; Indels

0; Gaps

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Page 5

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
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 length: 0
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131.295 Million cell updates/sec
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| cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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WIDPENGDSGYAPKFQG 17
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      1 US-08-017-570-4
US-08-017-570-6
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1 US-09-672-609-1
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Sequence 57, Appl	•	•	Sequence 89, Appl	•	-	Sequence 79, Appl	•	•	•	Sequence 31, Appl	•	•	•	Sequence 16, Appl	Sequence 38, Appl	•	Sequence 6, Appli

ALIGNMENTS

RESULT 1 US-08-017-570-4

Sequence 4, Application US/08017570
Patent No. 5472693

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION UNUMER: US/08/017,570
FILING DATE: 19930216
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
TELEPONEUNICATION INFORMATION:
TELEPONEUNICATION INFORMATION:
TELEPONEUNICATION OF SEQ ID NO: 4:

TELEPONEUNICATION SEQ ID NO: 4:
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                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-017-570-4
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                                                                        Query Match
Best'Local S
Matches 15
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APPLICANT: GOURLIE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: MEZES, PETER S

APPLICANT: KAPLAN, DONALD A

APPLICANT: KAPLAN, DONALD A

APPLICANT: SCHLOM, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. U
STREET: P.O. Box 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 48641-1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Midland
                                                                          Local Similarity 88.2 es 15; Conservative
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WIDPENGDTEYAPKFOG
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Pred. No. 5.
                                                                          Mismatches
                                                                                                                DB 1;
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Best Local
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REFERECE/DOCKET NUMBER: C-Je
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                    tent No.
                                                                                                                                APPLICANT:
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NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINGEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
                                                                CORRESPONDENCE ADDRESS:
                                                                                   NUMBER OF SEQUENCES:
                                                                                               TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
                                                                                                                                                                   APPLICANT:
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             CITY: Midland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/017,570 FILING DATE: 19930216 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                STREET:
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Similarity 88.2%;
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                               P.O. Box 1967
                                                                                                                                  SCHLOM, JEFFREY
                                                                                                                                                                                GOURLIE, BRIAN B
RIXON, MARK W
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MEZES, PETER S
KAPLAN, DONALD
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KAPLAN, DONALD A
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                                                Duane
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Pred. No.
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US-08-471-426-6
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Best Local Similarity 88.7
Matches 15; Conservative
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,570
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,77
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: GOURLI
APPLICANT: RIXON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
FILING DATE: 06-UN-1995
CIACCETTATION: E16
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,570
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TOPOLOGY:
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STREET: P.
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REFERENCE/DOCKET NUMBER:
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KAPLAN, DONALD A
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VENTION: A NOVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIXON, MARK W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOURLIE,
                                                                                                                                                                                                                                                                                                                                                                                          Duane C. Ul
O. Box 1967
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88.2%; Pred. No. 5.
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                     C-38,777
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US-09-672-609-3
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US-09-672-609-1
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US-09-672-609-1
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Best Local Similarity 88.2%;
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APPLICANT:
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PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
                                                 FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
         PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
                                                                                                             APPLICANT:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 124
                                                                                              PHICANT: Armour, Kathryn
TLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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TYPE: amino acid
TOPOLOGY: linear
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les 15; Conserv
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                                                                                                                         Harris, William J.
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Pred. No. 5.
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Best Local S
Matches 15
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Sequence 4, App. _____
Sequence 4, App. _____
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Best Local
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APPLICANT: 7
APPLICANT: 6
APPLICANT: 6
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PRIOR FILING DATE: 198-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
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CURRENT FILING DATE: 2000-09-28
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APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
                                                     APPLICANT: Armour, TITLE OF INVENTION:
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                                     FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
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LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRS, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
OCHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
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LOCATION: 1..124
COTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRS, murine COL-1 VH CDRs, and Phe-27, Asn-28,
OCHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
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Local Similarity 88.2%;
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Tempest, Philip R.
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                                                                                       Harris, William J.
                                                                                                                 Carr, Frank J.
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High Affinity Humanized Anti-CEA Monoclonal Antibodies
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Pred. No. 5.3e-07;
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Pred. No. 5.3e-07;
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RESULT 10
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US-09-672-609-6
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                                   Sequence 7, Application US/09672609
PATENT AGO: 6333405
GENERAL! INFORMATION:
APPLICANT: Anderson, W.H. Kerr
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Best Local (
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Best Local :
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CÜRRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
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APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized
                      APPLICANT:
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PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
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OTHER INFORMATION: Humanized heavy chain variable region containing OTHER INFORMATION: NEWM VH FRB, murine COL-1 VH CDRB, and Ala-24, Ph OTHER INFORMATION: Ile-29, Lys-30, Ala-79, Asn-97, and Thr-98
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NAME/KEY: Humanized COL-1 VH, HuVHAA
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OTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
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Anderson, W.H. Ker
Tempest, Philip R.
Carr, Frank J.
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Tempest, Philip R.
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Pred. No. 5.3e-07;
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Pred. No. 5.3e-07;
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SEQ ID NO 8
                                                                                                                                        Matches
                                                                                                                                                                                                     Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
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PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
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CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
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FEATURE:
RAME/KEY: Humanized COL-1 VH, HuVHAY
LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region contain of the companion of the color of the color
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TYPE: PRT
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SOFTWARE: Microsoft Word 97 SR-2
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                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Humanized heavy chain variable region contagning human OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala 24, Phe-27, Asn OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn; 97, and Thr-98
                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHATAY
LOCATION: 1..124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 124
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                     Match 89.1%;
Local Similarity 88.2%;
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                                                                1 WIDPENGDSGYAPKFQG 17
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WIDPENGDTEYAPKFQG
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Harris, William J.
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                                                                                                                                        Conservative
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88.2%;
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Pred. No. 5.3e-07;
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Pred. No. 5.3e-07;
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US-09-672-609-9

Sequence 9, Application US/09672609 Patent No. 6333405

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RESULT 13
US-09-672-609-10
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Best Local S
Matches 15
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CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
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PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word
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TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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                                                                                                                                                     NAME/KEY: Humanized COL-1 VH, HuVHT
LOCATION: 1..124
COTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
OTHER INFORMATION: Ile-29, Lys-30, Thr-72, Asn-97, and Thr-98
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                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
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NAME/KEY: Humanized COL-1 VH, HuVHASTAY
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Harris, William J.
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                                                                      Conservative
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Pred. No. 5.3e-07;
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Pred. No.
                                                                      Mismatches
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; OTHER INFORMATION: US-09-672-609-12
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US-09-672-609-12
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US-09-672-609-11
                                                                                                                                                                                    SOFTWARE: Mic. SEQ ID NO 12
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FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
CURRENT FILING DATE: 09/025,403
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
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APPLICANT: Armour,
TITLE OF INVENTION:
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PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
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ORGANISM: Artificial Sequence
PEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHS
LOCATION: 1..124
              OTHER INFORMATION: Humanized heavy chain variable region expressed from ATCC OTHER INFORMATION: CRL-12208, and containing human NEWM VH FRs, murine COL-1 VOTHER INFORMATION: and phe-27, Asn-28, Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, OTHER INFORMATION: Tyr-80, Asn-97, and Thr-98
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                                                                                          FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHSTAY
LOCATION: 1..124
                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                      TYPE: PRT
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Tempest, Philip R.
Carr, Frank J.
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Kathryn
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Kathryn
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Pred. No. 5.3e-07;
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89.1%;

Score 90;

BB 4

Length 124;

CDRs

밁 Search completed: July 30, 2003, 09:38:27 Job time: 5.4784 secs Best Local Similarity 88.2%; Pred. No. 5.3e-07; Matches 15; Conservative 1; Mismatches 1; Indels 1 WIDPENGDSGYAPKFQG 17
|||||||: |||||||
50 WIDPENGDTEYAPKFQG 66 0; Gaps 0;

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OM protein - protein search, using sw model
                                           8
                                       July 30, 2003, 09:31:34 ; Search time 2.36545 Seconds
                                                                                                                                             Copyright
                                                                                                                                           GenCore version (c) 1993 - 2003
(without alignments)
325.245 Million cell updates/sec
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Compugen Ltd.
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Perfect score: US-09-865-198-3 51 YYGDYEGY 8

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 2000000000 length: 0

Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45

summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:* 32.

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

U	4	ω	ເ	ï	0	9	œ	7	ā	úī	4	ώ	N	-	0
35	35	ω 5	35	35		35		S S	ω 5	35	36	36	36	36	36
68.6	68.6	68.6	68.6	68.6	68.6	68.6	68.6	68.6	68.6	68.6	70.6	70.6	70.6	70.6	70.6
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۲	N	N	N	N	N	N	N	N	N	N	μ	_	μ	N	N
I61573	D71003	A75128	T14243	869529	H85910	H91066	AB1210	S03844	S16280	G82387	TIUHGO	S07047	JN0550	A84518	TS1545
homeotic protein l	probable transamin	probable transamin	ubiquinol-cytochro	hypothetical prote	unknown protein en	hypothetical prote	dTDP-sugar epimera	Ig heavy chain pre	Ig heavy chain (38	hypothetical prote	iodide peroxidase	iodide peroxidase	iodide peroxidase	probable receptor-	receptor protein k

ALIGNMENTS

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000 hypothetical protein Cj1295 [imported] - Campylobacter jejuni (strain NCTC 11168) C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002 C;Accession: D81272 맑 á A;Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73722.1; PID:g696872 A;Experimental source: serotype O2, strain NCTC 11168 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype; A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: D91272 C; Superfamily: Campylobacter jejuni hypothetical protein Cj1295 A;Gene: Cj1295 A; Cross-references: GB: AL139078; A; Molecule type: DNA A; Status: preliminary A;Residues: 1-435 <PAR> Genetics: Matches Query Match Best Local Similarity
Matches 6; Conserv 325 YGDYDGY 331 2 YGDYEGY 8 Conservative 80.4**%**; 85.7**%**; Pred. No. 14; 1; Mismatches 2; 0 Length 435; Indels o , Gaps 0,

MPA43 protein - yeast (Saccharomyces cerevisiae) N;Alternate names: protein N0875; protein YNL249 protein YNL249c

C;Species: Saccharomyces cerevisiae C;Date: 27-Apr.1996 #sequence_revision 03-May-1996 #text_change 06-Feb-1998

C; Accession:

S63222;

 R_i Sen-Gupta, M.; Gueldener, U.; Beinhauer, J.; Fiedler, T.; Hegemann, J.H. submitted to the Protein Sequence Database, April 1996

A;Reference number: S63220
A;Accession: S63222
A;Molecule type: DNA

A;Residues: 1-542 <SEN>
A;Cross-references: EMBL:Z71525; NID:g1302290; PID:e239640; PID:g1302291; MIPS:YNL249c A;Experimental source: strain S288C
A;Boles, E.; Hettmann, C.; Zimmermann, F.K.
submitted to the EMBL Data Library, December 1995
A;Reference number: S61594

A; Accession: S61594

A;Molecule type: DNA
A;Residues: 'YQD',45,'SR',48,'HGNLA',54-542 <BOL>
A;Cross-references: EMBL:X34214; NID:g1122898; PID:e214032; PID:g1122899

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C; Genetics:
A; Gene: SGD: MPA43
A; Cross-references: SA; Cross-re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 15-Oct-1999 #sequence_revision C;Accession: T18444
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C;Superfamily: methionyl-tRNA synthetase, dimer-forming
C;Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase;
F;13,19,50,300/Active site: Tyr, His, Asp, Lys #status predicto
                                                                                                                                                                                                                                                       A;Note: C0385c
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A;Accession: T18444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Lawson, D.; Bowman, S.; Barrell, submitted to the EMBL Data Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M64273; GB:J05744; NID:g155135; PIDN:AAA27510.1; A;Experimental source: strain HB8, ATCC 27634
A;Note: the authors translated the codon TAC for residue 323 as Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Mclecule type: DNA
A;Residues: 1-616 <NUR>
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J. Biol. Chem. 266, 3268-3277, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Dec-2002 C;Accession: A39517
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                                                                                                         Query Match
Best Local, Similarity
Matches ;6; Conserv
                                                                                                                                                                                                                                                                                Map position: 3; Introns: 1597/3; 1625/3
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YFDDYEGY 532
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75.0%;
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85.7%;
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                                                                                                                         Score 40; DB
Pred. No. 78;
1; Mismatches
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Y, August 1997
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Pred. No.
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Pred. No.
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C;Species: Caenorhabo
C;Date: 20-Feb-1995 #
C;Accession: S44634
R;Anderson, K
                                                                                                                                                                                                            RESULT
E83656
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-660 <STO
                                                                                                                                                    methionyl-tRNA synthetase metS [imported] - Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data A; Description: Sequence of A; Reference number: $44628
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                                                  A; Reference number: A; Accession: E83656
                                                                                                R; Takami, H.; Nakasone,
Nucleic Acids Res. 28, 4
                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: ac 1185
C;SuperfamIly: Aquifex aeolicus hypothetical protein ac 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid
A;Molecule type: DNA
A;Residues: 1-595 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein aq 1185 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 04-Mar-2000
C;Accession: B70402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S446
                                                                                  A; Title: Complete genome
                                                                                                                                    C; Accession: E83656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE000727; NID:g2983623; PIDN:AAC07204.1; PID:g2983636; GB:AE00065
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: The complete genome A; Reference number: A70300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B70402
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A; Residues: 1-63 < AND>
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Best Local Similarity
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Caenorhabditis elegans
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                                                                                                    28, 4317-4331,
                                                                    A83650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.V.; Gaasterland,
                                                                                                                                                                                                                                                                                                                                                                 74.5%;
85.7%;
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75.0%;
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the C. elegans cosmid
                                                                                                                    Takaki, Y.; Maeno,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e of the hyperthermophilic bacterium MUID:98196666; PMID:9537320
                                                                    MUID:20512582;
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Pred. No.
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Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence not shown; translation
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                                                                                    the alkaliphilic bacterium
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                                                                                                                                                                                                                                                                                                                                                             DB
62;
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                                                                                                                  Sasaki, R.; Masui, N.; Fuji, F.; Hira
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                                                                                                                                                        23-Dec-2002
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A;Gene: metS
C;Superfamily: methionyl-tRNA synthetase, dimer-forming
                                                                                                                                                                                                                                                                                                                        hypothetical protein C37A5.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T19805
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A;Title: The complete genome sequence of the murine respiratory pathogen A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: C90538
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A;Experimental source: strain C-125
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                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-89 <WIL>
                                                                                                                                                                                                                                                                           submitted to the EMBL Data A; Reference number: Z19180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-3216 <KUR>
A; Cross-references: GB:AL445566; PID:g14089624; PIDN:CAC13384.1; GSPDB:GN00153
                                                                                                                                                                                                                                                                A; Accession: T19805
                                                                                                                                                                                                                                                                                                         R;White, S.
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                                                           Query Match
Best Local S
Matches 6
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Matches
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                                                                                                                                                                                                EMBL: Z92828; PIDN: CAB07335.1; GSPDB: GN00019; CESP: C37A5.8
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                                                                        Score 37;
Pred. No.
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                                                                                      Length 89;
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RESULT 12
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                                                                       A;Reference number: S38097
A;Accession: S38115
A;Molecula
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A69012
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A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13688
                                             A; Molecule type: DNA
A; Residues: 1-271 < URR>
                                                                                                                                   R;Urrestarazu, L.A.; Jauniaux, J.C. submitted to the Protein Sequence D
                                                                                                                                                                                  C;Date: 03-May-1994 #sequence_revision
C;Accession: S38115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: uncharacterized conserved protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE000879; GB:AE000666; NID:g2622175; PIDN:AAB85580.1; PID:g262219
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta A;Reference number: A69000; MUID:98037514; PMID:9371463 A;Accession: A69012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;10-93/Domain: immunoglobulin homology
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-110 < PEN>
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C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C;Accession: S13688
A;Cross-references: EMBL:Z28268; NID:g486490; PID:g486491; A;Experimental source: strain S288C
                                                                                                                                                                                                                                                   hypothetical protein YKR043c - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: MTH1091
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Best Local S
Matches 5
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                                                                                                                                                                                                                             Species: Saccharomyces cerevisiae
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                                                                                                                                       March
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GSPDB:GN00011; MIPS:YKR043c

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RESULT 14
881105
ABC transporter, ATP-binding protein NMB1240 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: 1
R; Parkhill, J
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A;Gene: MIPS:YKR043C
A;Crose-references: SGD:S0001751
A;Map position: 11R
C;Superfamily: phosphoglycerate mutase; phosphoglycerate mutase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                           R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen, Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily:
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A;Gene: NMA1409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable ABC-transporter ATP-binding protein NMA1409 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
                                                                                                                                                                                ;Residues: 1-542 <TET>
;Cross-references: GB:AE002472;
;Experimental source: serogroup
                                                                                                                       ;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Residues: 1-542 <PAR>;Residues: 1-542 <PAR>;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742;
                                            Matches
                                                          Query Match
Best Local'Similarity
                                                                                                                                                                                                                                                                 Status: preliminary
                                                                                                                                                                                                                                                                                  Title: Complete genome sequence of Neisseria meningitidis serogroup B Reference number: A81000; MUID:20175755; PMID:10710307 Accession: E81105
                                                                                                                                                                                                                                                                                                                                             Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                                                            Gene: NMB1240
                                                                                                                                                                                                                                            Molecule type: DNA
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T26053
Search completed: July 30, 2003, 09:44:07 Job time: 6.36545 secs
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                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A;Reference number: Z20143
A;Accession: T26053
                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein W01C9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                         A; Introns: 30/1; 64/1; 100/3; 124/3; 229/3; 272/3;
                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z49969; PIDN:CAA90270.1; GSPDB:GN00020; CESP:W01C9.2 A;Experimental source: clone W01C9
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                                                                                                                                         Matches
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Best Local
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Post-processing: Minimum Match 0%
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Copyright (c) 1993 - 2003
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ASSY METAC
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SOX8 HUMAN
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GGT BACSU
ACGA RHOCA
PERT HUMAN
K6PP PASMU
YO23 BPHPI
LYS MOUSE
LHX1 BRARE
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2 bacillus su
7 rattus nory
8 mosteurella
2 bacteriopha
6 rattus nory
9 mus musculu
6 brachydanio
6 homo sapien
6 kluyveromyc
1 bacillus su
1 saccharomyc
1 sarchaeoglob
8 thermoanaer
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8 bacillus ha
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thermus the
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ProDom; PD000094; LIM; 2.
SWART; SM00389; HOX; 1.
SMART; SM00132; LIM; 2.
PROSITE; PS00027; HOMEOBOX_1;
PROSITE; PS50071; HOMEOBOX_2;
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Result No.

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Database

Minimum DB Maximum DB

Searched:

Sequence:

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Q9m7t0 a	P03949	P06226 1	Q9qzz4 1	P94972 r	P40657 (Q8yaf2	Q92f90	Q8ny00 s	Q99wb3 s	P23920 1	067298 a	
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ALIGNMENTS

RESULT	5 HUMAN
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P	(Rel. 40, Creat
1	(Rel. 40, Last sequence up
DE UT	28-FEB-2003 (Rel. 41, Last annotation update)
9 5	P. C. C. L.
လွှ မ	Homo sapiens (Human).
8	hordata;
8	ia; Primates; Catarrhini; Hominidae;
8	D=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	1137295;
3 3	chromogomal localization and commogration of
R 7	"Genomic structure, chromosomar iocalization and expression of the
P.	Gene 260:95-101(2000).
S	FUNCTION: Plays an essential role in the regulation of r
റ്റ	development of the
38	nervous system.
88	-i- TISSUE SPECIFICITY: Expressed in fetal brain and in various
8	. 2
36	-
25	-i- SIMILARITY: Contains 2 LIM zinc-binding domains.
റ്റ	
გ	ROT entry is copyright. It is produced thr
ရှိ	between the Swiss Institute of Bioinformatics and the EMBL outstation -
8	on
3 2	use by non-profit institutions as long as its content is in no way
38	modified and this statement is not removed. Usage by and for commercial
3 8	entities requires a license agreement (see nttp://www.isb-sib.cn/announce/ or send an email to license@ish-sib.ch)
გ მ	111111111111111111111111111111111111111
DR	AF291181; AAG36963.1;
DR	
DR	TRANSFAC; T04180;
DR	Genew; HGNC:14216; LHX5.
DR	MIM; 605992;
DR	
D R	GO; GO:0007417; P:central nervous system development; ISS.
	Interpro; IPROUIS56; HomeoDox.
3 5	THICKERIO, TEROUTION, TIM COMPO
ב א	Pfam: PR00046; homeobox: 1.
DR S	PF00412; LIM;
DR	n, PD000010; H
2	DECORPORE DICCORDA . T.T. C.

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RESULT
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Best Local
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                                                                   TRANSFAC; T04209; ...
InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LIM.
InterPro; IPR007107; LIM. homeo.
Pfam; PF00046; homeobox; 1.
Pfam; PF000412; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00478; LIM DOMAIN 1; 2.
PROSITE; PS50023; LIM DOMAIN 2; 2.
Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Transcription regulation.
DOMAIN 61 LIM 1.
DOMAIN 62 125 LIM 2.
DOMAIN 63 125 LIM 2.
DOMAIN 64 125 LIM 2.
DOMAIN 65 125 LIM 2.
DOMAIN 67 125 LIM 2.
DOMAIN 68 125 LIM 2.
DOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XENLA
                                                                                                                                                                                                                     EMBL; L42546; AAA99464.1; -.
EMBL; Z11587; CAA77672.1; -.
HSSP; P06601; IFJL.
                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 188-225 FROM N.A.

MEDLINE=92192449; PubMed=1347750;

Taira M., Jamrich M., Good P.J., Dawid I.B.;

"The LIM domain-containing homeo box gene Xlim-1

specifically in the organizer region of Xenopus

Genes Dev. 6:356-366(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1994 (Rel. 30, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
LIM/homeobox protein Lhx5 (Homeobox protein LIM-5) (XLIM-5)
LHX5 OR LIM5 OR LIM2A OR LIM-2A.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
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MEDLINE-95377545; PubMed=7649385;

Toyama R., Curtiss P.E., Otani H.,

Toyama R., Curtiss P.E., Otani H.,

"The LIM class homeobox gene lim5:

Xenopus and zebrafish.";

Dev. Biol. 170:583-593(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopos.
                    ProDom; PD000010; Homeobox; 1. ProDom; PD600094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Contains 1 homeobox domain.
SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BEV. 6:356-366(1992/).
FUNCTION: PROBABLY INVOLVED I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYGDYQG 284
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180
402 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
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Pred. No. 8.4;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN THE PATTERNING OF THE NERVOUS EARLY SPECIFICATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kimura M., Dawid I.B., Taira M.; implied role in CNS patterning i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402
                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xlim-1 is expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 402;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gastrula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
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RESULT 3
MP43_YEAS
ID MP43
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Best Local S
Matches 6
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Best Local S
Matches 6
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01-OCT-1996 (Rel. 34, Last
30-MAY-2000 (Rel. 39, Last
MPA43 protein.
MPA43 OR YNL249C OR N0875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MP43 YEAST
P53583;
                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                        SGD;
                                                                                                                                                                                                        EMBL; X96722; CAA65495.1; -.
EMBL; Z71525; CAA96156.1; -.
EMBL; X94214; CAA63905.1; -.
PIR; S63222; S63222.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boles E., Hettmann C., Zimmermann F.K.; Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of the 33 kb long region between ORC5 and SUI1 from the left arm of chromosome XIV from Saccharomyces cerevisiae."; Yeast 13:849-860(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS00023; LIM_DOMAIN_2; 2.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00027; HOMEOBOX_2; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX_2; 1.
Repeat; LIM domain; Metal-binding; Zinc; Transcription regulat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ENY.WA-1A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97377992; PubMed=9234673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288c
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Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                 6,
                                                                      Similarity
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    YYGDYEG 7
                                                                                                                                      46
542 AA;
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. 34, Last sequence . 39, Last annotation.
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61667
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85.7%;
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85.7%;
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                                               Score 40; DB
Pred. No. 16;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41;
Pred. No.
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. 16;
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                                                                                         Length 542;
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RESULT 4
SYM THEM
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ID SYM
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DT 
EMBL; M64273; AAA27510.1; -.

DR PDB; 1ABH; 04-MAY-99.

R PDB; 1ABH; 04-MAY-99.

R HAMAP; MF 01228; fused; 1.

DR InterPro; IPR00495; MetG Cterm.

InterPro; IPR00430; tRNA-synt_1a.

InterPro; IPR002300; tRNA-synt_I.

R InterPro; IPR002304; tRNA-synt_I.

DR InterPro; IPR00234; tRNA-synt_I.

DR InterPro; IPR00234; tRNA-synt_I.

DR Ffam; PF00133; tRNA-synt_I.

DR Pfam; PF00133; tRNA-synt_I.

DR Pfam; PF01588; tRNA-bind; 1.

DR Pfam; PF01588; tRNA-bind; 1.

DR Pfam; PF01588; tRNA-SynTHMET.

DR PROSTS; PRRSF001528; MetRS dimerising; 1.

DR PROSTS; PRRSF00139; metG C term; 1.

DR TICRFAMS; TIGR00399; metG C term; 1.

DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.

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R. STRAINHEB / ATCC 27634;

R. STRAINHEB / ATCC 27634;

R. MEDLINE=20139706; PubMed=10673435;

R. MEDLINE=20139706; PubMed=10673435;

R. MITCHARMAN R., Wareki O., Ugaji-Yoshikawa Y., Kuwabara S., Shimada A.,

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Kuwabara S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Kuwabara S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Kuwabara S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Kuwabara S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Kuwabara S., Kumabara S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Kuwabara S., Kumabara S., Konno M.;

R. Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Kuwabara S., Kumabara S., Ku
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SYM THETH

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SYM THETH

P23 395;

01-NOV-1991 (Rel. 20, Created)

01-NOV-1991 (Rel. 20, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)

(MetRS).

METG OR METS.
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=HB8 / ATCC 27634;
MEDLINE=91131636; PubMed=1993699;
Nureki O., Muramateu T., Suzuki K., Kohda D., Matsuzawa H.,
Ohta T., Miyazawa T., Yokoyama S.;
"Methionyl-ENNA synthetase gene from an extreme thermophile, Ther
thermophilus HB8. Molecular cloning, primary-structure analysis,
expression in Escherichia coli, and site-directed mutagenesis.";
J., Biol. Chem. 266:3268-3277(1991).
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Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
MetG subfamily 2A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson J.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Sans M., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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                                                                                                                                                                                                                                                      WormPep;
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01-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
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Rhabditidae; Pelode:
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6; Conserva
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  YYGGYNGY 63
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                                                                                                    Conservative
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
L protein F22B7.4 in chromosome II
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3 AA; 68
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75.0%;
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Pred. No.
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RESULT 6
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RESULT 7
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28-FEB-2003 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q28793;
15-DEC-1998
15-DEC-1998
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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-I- FUNCTION: MAY PLAY A ROLE IN THE FORMATION AND REGULATION OF TIGHT JUNCTION (TJ) PARACELLULAR PERMEABILITY BARRIER. INTE
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01284; MARVEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U49183; AAC48565.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potorous tridactylus (Potoroo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Potoroidae; Potorous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH
EPITHELIAL AND ENDOTHELIAL CELLS.
DOMAIN: THE C-TERMINAL IS CYTOPLASMIC AND IS IMPORTANT FOR
INTERACTION WITH ZO-1. NECESSARY FOR THE TIGHT JUNCTION
LOCALIZATION. INVOLVED IN THE REGULATION OF THE PERMEABILITY
BARRIER FUNCTION OF THE TIGHT JUNCTION (BY SIMILARITY).
PTM: PHOSPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE ELL / OCCLUDIN FAMILY.
                               BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WITH ZO-1.
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(Rel. 37, Last sequence update)
(Rel. 39, Last annotation updat
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                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                OCCLUDIN.
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                                                                                                                                                                                                                        54075 MW;
                                                                                                                                                                            76.5%;
75.0%;
                                                                                                                                                                            Score 39; DB
Pred. No. 22;
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COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (PO
                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                                        4F0CA45A41094860 CRC64;
                                                                                                                                                              Mismatches
                               660 AA
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(See http://www.isb-sib@ch/announce/
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                                                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                Query Match
Best Local
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Pfam; PF01588; tRNA bind; 1.
PIRSF, PIRSF001528; MetRS dimerising; 1.
PRINTS; PR01041; TRNASYNTHMET.
TIGREAMS; TIGR00398; metG; 1.
TIGREAMS; TIGR00399; metG; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
PROSITE; PS50886; TRED; 1.
                                                                                                                                                                                                          DOMAIN
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF 01228; fused; 1.
InterPro; IPR004495; MetG_Cterm.
InterPro; IPR002300; tRNA-synt 1a.
InterPro; IPR00412; tRNA-synt T.
InterPro; IPR002304; tRNA-synt met.
InterPro; IPR002547; tRNA_bind.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP001507; BAB03772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           halodurans and genomic sequence comparison with Bacillus subtilis.";

Nucleic Acids Res. 28:4317-4331(2000).

-!- FUNCTION: Is required not only for elongation of protein synthesis but also for the initiation of all mRNA translation through initiator tRNA(fMet) aminoacylation (By similarity).

-!- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sa
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methionyl-tRNA
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                                                                                                                                                                                                                                                                            RNA-binding; tRNA-binding; SITE 15 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P23395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; E83656; E83656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the alkaliphilic
                                                                                                                                                                                                                                                                                                                        Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restruction of the swiss its content by non-profit institutions as long as its content if the swisses of the swisses o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetG subfamily 2B.
SIMILARITY: Contains 1 tRNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diphosphate + L-methionyl-tRNA(Met).
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR METS
121
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YLGDYEGW 128
                                              YYGDYEGY 8
                                                                                                                                                                                  311
560
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660 AA;
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75.0%;
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Last annotation update)
tase (EC 6.1.1.10) (Methionine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillales;
                                                                                                                                                                                    MW
                                                                                                                                                                                                                                                                          Complete proteome. "HIGH" REGION.
                                                                                                             Score 38;
Pred. No.
                                                                                                                                                                                  TRNA-BINDING.
ATP (BY SIMILARITY)
; EC3408645728A536
                                                                                                                                                                                                                                                    "KMSKS" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillaceae;
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                                                                                                                                   DB 1;
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., Kuhara S.
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th Bacillus subtilis.";
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                                                                                                                                   Length 660;
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RESULT 8
YK23_YEAST

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REQUENCE FROM LINE 2192760; PubMed=11932238;

RX MEDINE=2192760; PubMed=11932238;

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Linja J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Lingh J.A., Li W., Liu J., Muhite O., White R.H., de Macario E.C.,

RA Springer T.A., Umayam L.A., White O., White R.H., Paulsen I.,

RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

RA Ferry J.G., Jarrell K.F., Swanson R.V., Zinder S.H., Lander E.,
PROPERTY OF THE PROPERTY OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
ASSY_METAC
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Best Local :
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QBTNY5;
28-FEB-2003
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P36136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; / Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Euryarchaeota
Methanosarcinales; Methanosarcinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Argininosuccinate
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28-FEB-2003 (Rel.
15-SEP-2003 (Rel.
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SGD; S0001751; YKR043C.
InterPro; IPR001345; PG.
Pfam; PF00300; PGAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z28268; CAA82119.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Urrestarazu L.A., Jauniaux J.-C.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical YKR043C.
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                    and physiological diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanosarcina acetivorans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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42,
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; Saccharomycetaceae; Saccharomyces
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100.0%; Pred. No.
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996
01-OCT-1996
28-FEB-2003
EMBL; L42547;
HSSP; P06601;
                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD003544; ArginoBuc_synth; 1.
TIGRPAMS; TIGR00032; argG; I.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Ligase; ATP-binding; Comp.
SEQUENCE 394 AA; 43994 MW; 2B995B9C138E7EF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata,
Actinopterygii; Neopterygii;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-BB-2003 (Rel. 41, Last annotation update)
LIM/homeobox protein Lhx5 (Homeobox protein L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO01518; Arginosuc synth. Pfam, PF00764; Arginosuc synth; 1. ProDom; PD003544; Arginosuc synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=95377545; PubMed=7649385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                Kenopus and zebrafish.
                                                                                                                                                                                                                                                                                                                                                                                                                                    The LIM class homeobox gene lim5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE010900; AAM05540.1; -.
                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Contains 1 homeobox domain.
SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diphosphate + L-argininosuccinate. PATHWAY: Arginine biosynthesis; seven SUBUNIT: Homotetramer (By similarity)
                                                                                                                                                                                                                                                                                                                                                                       FUNCTION:
                                                                                                                                                                                                                                                                                                                         DIENCEPHALON.
                                                                                                                                                                                                                                                                                                                                             SYSTEM, IN PARTICULAR IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the argininosuccinate synthase
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                                                                                                                                                                                                                                                                                                                       170:583-593 (1995).
170:583-593 (1995).
ON: PROBABLY INVOLVED IN THE PATTERNING OF THE NERVOUS
IN PARTICULAR IN THE EARLY SPECIFICATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rerio (Zebrafish) (Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                   AAA99465.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata;
pterygii; Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.5%;
100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimura M., Dawid I.B., Taira M. implied role in CNS patterning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seventh step
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                                                                                                                           There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIM-5).
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                                                                                                                                                                                                   a collaboration
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RESULT 11
SOX8_HUMA
ID SOX8
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Best Local S
Matches 5
                                                                                                                  Ellington
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                               P57073; Q9NZW2;
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
15-SEP-2003 (Rel.
SEQUENCE OF 119-446 FROM N.A.

MEDLINE=20130119; PubMed=10662550;

Pfeifer D., Poulat F., Holinski-Feder E., Kooy F., Scherer G.;

"The SOX8 gene is located within 700 kb of the tip of chromosome l
and is deleted in a patient with ATR-16 syndrome.";

Genomics 63:108-116(2000).

-!- FUNCTION: MAY PLAY A ROLE IN CENTRAL NERVOUS SYSTEM, LIMB AND
PACIAL DEVELOPMENT. MAY BE INVOLVED IN MALE SEX DETERMINATION.

BINDS THE CONSENSUS MOTIF 5'-[AT][AT]CAA[AT]G-3' (BY SIMOLARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                    Hum. Mol.
                                                                                                                                                                                             Higgs D.R.;
                                                                                                                                                                                                      Daniels R.J.,
Tufarelli C.,
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Cheng Y.-C., Badge R.M., F. "SOX8: a newly identified
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                         AF
Of
                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                 Submitted (JAN-2000)
                                                                                                                                                                                                                                                                                      tumours and a candidate
                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00478; LIM DOMAIN 1;
PROSITE; PS50023; LIM DOMAIN 2;
PROSITE; PS00027; HOMEOBOX 1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000010; Homeobox;
ProDom; PD000094; LIM; 2.
SMART; SM00389; HOX; 1.
SMART; SM00133; LIM; 2.
                                                                                                                                                                                                                                MEDLINE=
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00046; homec Pfam; PF00412; LIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZFIN; ZDB-GENE-980526-484; lim5
                                                                                                                                                                                   Sequence, structure and pathology of the fully annotated terminal
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                                                                                                                                                                                                                                                                                                                                                        ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                              Genet.
                                                                                                                                                                         short arm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50071; HOMEOBOX 2; 1.

DNA-binding; Nuclear protein; Developmental protein;
IM domain; Metal-binding; Zinc; Transcription regulat
                                                                                                                  (FEB-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          399 AA;
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180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                        Peden J.F.,
Kearney L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homeobox; 1.
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239
                                                                                                                                                            arm of human chromosome 16."; 10:339-352(2001).
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                  the
                                                                                                                                                                                                                                                                                     , Armour J.A.L., Scottined human gene expressed for the mental retardat
                                                                                                                                                                                                       Lloyd C., Hos
Buckle V.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIM 2
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                                                                                                                                                                                                       Horsley S.W., Clark K.,
J., Doggett N.A., Flint
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pressed in
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                                                                                                                  databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 399;
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                                                                                                                                                                                                                                                                                                paediatric
                                                                                                                                                                                                                                                                                      phenotype
  DETERMINATION.
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043390;
16-OCT-2001
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EMBL; AE006465; AAK61260.1; -.
EMBL; Z99757; CAB75612.1; ALT INIT.
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                                                         This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GG; GO:0003702; F:RNA polymerase II transcription factor acti. . GO; GO:0007417; F:central nervous system development; TAS. GO; GO:006357; F:regulation of transcription from Pol II pro. . InterPro; IPR000910; HMG 12 box.

PFAm; PF00595; HMG box; I.
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                                            between
                                                                                                                          Nucleic Acids Res. 26:439-445 (1998).
-I- FUNCTION: COMPONENT OF RIBONUCLEOSOMES,
-LEAST 20 OTHER DIFFERENT HETEROGENIOUS N
(HNRNP). HNRNP PLAY AN IMPORTANT ROLE IN
                                                                                                                                                                                                                           Hassfeld W., Chan E.K.L.,
Steiner G., Tan E.M.;
                                                                                                                                                                                                                                                        MEDLINE=98083170;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                      Heterogeneous
                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50118; HMG BOX 2; 1.
Transcription regulation; DNA-binding; Nuclear protein.
DNA_BIND 102 170 HMG BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:11203; SOX8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                      hnRNP P.
                                                                                                                                                                                               "Molecular definition of heterogeneous nuclear ribonucleoprotein (hnRNP R) using autoimmune antibody: immunological relationship v
                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
        e European B
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                                                                                SUBCELLULAR LOCATION: Nuclear; nucleoplasm. SIMILARITY: Contains 3 RNA recognition moti
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                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - the Swiss Institute of Bioinformatics are no restrictions on its European Bioinformatics Institute. There are no restrictions on its
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75.0%;
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Last annotation update)
ribonucleoprotein R (hnRNP
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P34115;
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SMART; SM00360; RRM; 3.

TIGREAMs; TIGR01648; hnRNP-R-Q;
PROSITE; PS50102; RRM; 3.

PROSITE; PS00030; RRM RNP 1; 2.
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GO; GO:0008436; F:heterogeneous nuclear ribonucleoprotein; TAS.
GO; GO:0003723; F:RNA binding activity; TAS.
GO; GO:0006397; P:mRNA processing; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                              "Molecular cloning and characterization of two genes encoding a cell surface glycoprotein involved in the sexual cell fusion Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                01-FEB-1994
28-FEB-2003
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PIR; T02673; T02673.
HSSP; P09651; 1HA1.
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or send an email to license@isb-sib.ch).
                                                             Dev. Biol. 156:201-208(1993).
-I- FUNCTION: INVOLVED IN THE SEXUAL
-I- SUBCELLULAR LOCATION: Attached to
-I- DEVELOPMENTAL STAGE: EXPRESSED AT
                                                                                                                                                    Fang H., Higa M.,
                                                                                                                                                                MEDLINE=93193972;
                                                                                                                                                                               STRAIN=AX3;
                                                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                                                               Eukaryota; Mycetozoa;
                                                                                                                                                                                                                                           Dictyostelium discoideum
                                                                                                                                                                                                                                                                     Cell surface
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InterPro; IPR000504; RNA_rec_mot.
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                                                                                                                                                                                                                  NCBI_TaxID=44689;
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FUSION COMPETENCE OF CELLS.

PTM: THE SUGAR CHAINS MAY PLAY IMPORTANT ROLES IN CELL FUSION PTM: The GPI-anchor contains a phosphoceramide moiety.

MISCELLANGOUS: GPI38A EXPRESSION IS MUCH HIGHER THAN THAT OF GP138B AND MAY WELL BE THE MAJOR GENE FOR GP138 PRODUCT.
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                      Suzuki K., Aiba K., Urushihara H., Yanagisawa K.
                                                                                                                                                                PubMed=7680629;
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3 X 11 AA APPROXIMATE
G-Y-D-Y-H-D-Y.
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Pred. No.
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RNA-BINDING (RRM)
RNA-BINDING (RRM)
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                                                                                                          01-OCT-1996
01-OCT-1996
28-FEB-2003
"Identification, sequence, and expression of t
glutamyltranspeptidase in Bacillus subtilis.",
J. Bacteriol. 178:4319-4322(1996).
                                                                                                                                GGT_BACSU
P54422;
                                    SEQUENCE FROM N.A.
STRAIN=168 / JH642;
MEDLINE=96312380; PubMed=8763966;
                                                                           Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                           Gamma-glutamyltranspeptidase GGT.
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InterPro; IPR002909;
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                              Strauch M.A.;
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Last annotation (EC 2.3.2.2))
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Choi S.K., Devine K.M., Dusterboft A., Ehrlich S.D., Emmerson P.T., RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Galleron N., RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N., RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Harwood C.R., Henaut A., RA Ghim S.Y., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Albin K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., RA Seiguchi J., Seconi E., Takagi T., Takahashi H., Takemaru K., RA Seto T., Scanlan E., Schletch S., Schroeter R., Scoffene F., Schletch S., Schroeter R., Scoffene F., Sein B.S., Soldo B., Rasto V., Winhama S., Vandenbol M., Vannier F., Vassarotti A., RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., Tane Complete genome sequence of the Gram-positive bacterium Bacillus
REPRESENTATION OF THE PROPERTY OF THE PROPERTY
                                                                                                MEROPS; TO3.001; -.

MEROPS; TO3.001; -.

BG11838; ggt.

InterPro; IPR000101; Gglutrnspptdase.

Pfam; PF01019; Gglu transpept; 1.

PRINTS; PR01210; GGTRANSPTASE.
                                                                                                                                                                                                                                                                                                                        EMBL; U49358; AAC44233.1;
EMBL; Z99113; CAB13724.1;
EMBL; Z99114; CAB13734.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as lost content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ogawa Y., Hosoyama H., Hamano M., Mot
"Purification and properties of gamma
Bacillus subtilis (natto).";
Agric Biol Chem. 55:2971-2977(1991)
                                                                                                                                                                                                                                                       MEROPS; T03.001;
                                                                                                                                                                                                                                                                                         PIR; F69631; F69631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=NR-1
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STRAIN=168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: (5-L-glutamyl)-peptide + an amino acid peptide + 5-L-glutamyl-amino acid.

ENZYME REGULATION: INHIBITED BY GLUCOSE.

PATHWAY: GGT PLAYS A KEY ROLE IN THE GAMMA-GLUTAMYL CYCLE, PATHWAY: FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHIONE.

SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WHE SYNTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: EXPRESSED AT THE END OF VEGETATIVE GROWTH. SIMILARITY: STRONG, TO OTHER GGT ENZYMES AND TO GL-7ACA ACYLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Secreted.
DEVELOPMENTAL STAGE: EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF 36-52 AND 403-442, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma-glutamyltranspeptidase from
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TIGRFAMs; TIGR00066; g_glut_trans; 1.
PROSITE; PS00462; G_GLU_TRANSPEPTIDASE; 1.

Acyltransferase; Signal; Glutathione biosynthesis;

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Search completed: July 30, 2003, 09:45:02 Job time: 4.24917 secs
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ACSA_RHOCA
                                                                                                         Query Match
Best Local S
Matches 5
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Best Local Similarity
Matches 5; Conserv
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CONFLICT
SEQUENCE
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SIGNAL,
CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACSA_RHOCA STANDARD; PRT; 656 AA.

068040;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-
                                                                                                                                                               Ligase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-SB1003 / St Louis;
STRAIN-SB1003 / St Louis;
MEDILINE=97404404; PubMed=9256491;
Vlcek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstei
"Sequence of a 189-kb segment of the chromosome of Rhodobacter
                                                                                                                                                                                    PIR; T03473; T03473; AMP-bind. InterPro; IPR00873; AMP-binding; 1. Pfam; PF00501; AMP-binding; 1. PRINTS; PR00154; AMPBINDING. PROSITE; PS00455; AMP_BINDING; 1.
                                                                                                                                                                                                                                                            EMBL; AF010496; AAC16126.1; -.
                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                     capsulatus SB1003.";
Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
-!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                             acetyl-CoA.
SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
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                                                      495
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                                                                              1 УХСОХЕСУ 8
                                                                                                         Similarity 5; Conserv
                                            |:| | ||
| YFGQYRGY 502
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403
467
46
587 AA;
                                                                                                      70.6%; nilarity 62.5%; Conservative
                                                                                                                                                              656 AA;
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402
587
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Pred. No.
                                                                                                       Score 36; DB 1; Length 656; Pred. No. 92; 1; Mismatches 2; Indels
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GAMMA-GLUTAMYLTRANSPEPTIDASE LARGE CHAIN.

GAMMA-GLUTAMYLTRANSPEPTIDASE SMALL CHAIN.

GAMMA-GLUTAMYL (POTENTIAL).

D -> V (IN REF. 3).

6BF200CBA882C4F6 CRC64;
                                                                                                                                                              706EA969331D71C2 CRC64;
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                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 587; 83;
                                                                                                                                                                                                                                                                                                                             as its content
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Maximum Match 100%
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1: sp archea:*
2: sp bacteria
3: sp fungi:*
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5: sp inverteb:
6: sp mammal:*
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9: sp phage:*
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333.364 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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51
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Copyright (c) 1993 - 2003 Compugen Ltd.
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5 Q8PEY8
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5 Q9PN04
5 Q9PN04
0 Q9LEB4
077328
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007245
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Q8H9T7
062093
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Q8pt44 methanosarc
Q8pey8 xanthomonas
Q8p3y0 xanthomonas
Q9pn04 campylobact
Q9leb4 nicotiana p
Q77328 plasmodium
Q8epa0 oceanobacil
Q8j5u5 bifidobacte
Q8ij27 plasmodium
Q8tj97 methanosarc
Q9fpj8 arabidopsis
Q9ffu0 arabidopsis
Q9ffu0 arabidopsis
Q67245 aquifex aeo
Q98qz9 mycoplasma
Q8h9t7 pseudomonas
Q8h9t7 pseudomonas
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4 5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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70.6	70.6	•	70.6	70.6	70.6	70.6	70.6	70.6		72.5		72.5			72.5	72.5			72.5		72.5		72.5			72.5		72.5
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Q9LX71	Q9V5P1	Q8SZN5	.Q8BL81	Q8BXC4	Q8TTD1	Q8TL35	Q97S13	Q8Y7X0	Q92CQ8	P90761	Q9BV64	Q8VHM5	Q96XC8	Q99KG1	Q23118	Q9JUB3	Q9JZ89	Q9H7I9	Q8BL32	Q8MZF7	Q9W098	Q8GJ09	Q8VVN1	Q8MZ31	Q9W0H1	Q8IRH6	027163	Q9U601
Q91x71 arabidopsis	Q9v5p1 drosophila	Q8szn5 drosophila	Q8bl81 mus musculu	Q8bxc4 mus musculu	Q8ttd1 methanosarc	-	Q97sl3 streptococc	Q8y7x0 listeria mo	Q92cq8 listeria in	caen		Q8vhm5 mus musculu	Q96xc8 sulfolobus	Q99kg1 mus musculu	Q23118 caenorhabdi	Q9jub3 neisseria m	Q9jz89 neisseria m	Q9h7i9 homo sapien			Q9w098 drosophila	Q8gj09 escherichia	Q8vvn1 vibrio chol	Q8mz31 drosophila		Q8irh6 drosophila	O27163 methanobact	Q9u601 anisakis si

ALIGNMENTS

RESULT 2

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RESULT ORBRIGHT OR RESULT 
P SQUIENCE FROM N.A.

P SQUIENCE FROM N.A.

(C STRAIN=ATCC 33913 / NCPPB 528;

(C STRAIN-ATCC 33913 / NCPPB 528;

(C STRA
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Q8P3J0;
01-OCT-2002
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MEDLINE=22022145; PubMed=12024217;
da Silva A.C.R., Ferro J.A., Reinach F.C., Far
Quaggio R.B., Monteiro-Vitorello C.B., Van Slu
Silva A.C.R., G. Amaral A.M., Berrolini M.C.,
Camarotte G. Camarara R. Cardon T. Chambar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical XCC4081.
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EMBL; AE012071; AAM39035.1; -.
Hypothetical protein; Complete
SEQUENCE 101 AA; 11468 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kanthomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kanthomonas
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Proteobacteria; Gammaproteobacteria;
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rel. 22, L
rel. 22, L
n XAC4200.
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ia; Gammaproteobacteria; Xanthomonadales;
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Sluys M.A.,
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Almeida N.F.,
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Almeida N.F.,
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Q9LEB4
ID EB4
ID Q9LE
AC Q9LE
DT 01-0
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DT 01-M
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OS Nico
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Q9PN04
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Matches 6
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                                                                         Q9LEB4
Q9LEB4;
Q1-OCT-2000
01-OCT-2000
01-MAR-2003
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01-DEC-2001 (
Hypothetical
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Q9PN04;
01-OCT-2000
Nicotiana plumbaginifolia (Leadwort-leaved tol
Bukaryota; Viridiplantae; Streptophyta; Embryv
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; lamiids; Solanales; Solanaceae; Ni
                                                   RBP45.
                                                              RNA binding
                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 4:
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20150912; PubMed=10688204; Parkhill J., Wren B.W., Mungall K., Basham D., Chillingworth T., Davies Jagels K., Karlyshev A.V., Moule S. Quail M.A., Ruther Whitherall M.A., Ruther Whitherall M.A., Ruther
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MEDLINE=20150912;
                                                                                                                                                                                                                                                                                                                      reveals hypervariable sequences.";
Nature 403:665-668(2000).
EMBL; AL139078; CAB73722.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Epsilon; Campylobacteraceae; Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE012531; AAM43302.1; -. Hypothetical protein; Complete SEQUENCE 101 AA; 11503 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                             'The genome sequence of the food-borne
                                                                                                                                                                                                                                                                                                                                                                         Whitehead S.,
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                                                                                                                                                                                                                                             Similarity 6; Conser
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                                                                                                                                                                                                                  YGDYEGY
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                                                                                                                                                                                                                                           80.4%;
nilarity 85.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                         Barrell B.G.
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49948 MW;
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75.0%;
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                                     (Leadwort-leaved tobacco)
                                                                                                                                                                                                                                           ; Score 41; DB;
; Pred. No. 48;
1; Mismatches
                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                   all K., Ketley J.M., Churcher C.,
Davies R.M., Feltwell T., Holroyd
onle S., Pallen M.J., Penn C.W.,
Rutherford K.M., van Vliet A.H.Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; I
Pred. No. 9
                                                                                                                                                                                                                                                                                              proteome.
1DFD6DDD270C0877
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578C1C9ED8E1404D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update)
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                                                                                                                                                                                                                                                                                                                                                             pathogen
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           Embryophyta; Tracheo edons; core eudicots;
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  Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                                                   J., Penn C.W.,
van Vliet A.H.Mg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>,,</u>
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                                                                                                                                                                                                                                                                     Length 435;
                                                                                                                                                                                                                                                                                               CRC64;
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                      Tracheophyta;
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                                                                                                        Lorkovic Z.J., Wieczorek Kirk D.A., Klahre U., Hemmings-Mieszczak M., Filipowicz W.;
Filipowicz W.;
"RBP45 and RBP47, two oligouridylate-specific hnRNP-like proteins interacting with poly(A)+ RNA in nuclei of plant cells.";
RNA 6:1610-1624(2000).
EMBL; AJ292767; CAC01237.1; -.
HSSP; P11940; 1CVJ.
ANU-2DPAGE; O9LEB4; -.
ANU-2DPAGE; O9LEB4; -.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PP0076; rrm; 3.
SMART; SM00360; RRM; 3.
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Bowman S., Lawson D., Basham D., Bowman S., Lawson D., Chillingworth T.,
Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby
Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
Mungall K., Murphy L., Oliver K., Oquail M.A., Rajandream M.-A.,
Rutter S., Skelton J., Squares R., Quares S., Sulston J.E.,
Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
"The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence
01-MAR-2003 (TrEMBLrel. 23, Last annotati
Putative serine/threonine protein kinase.
PFC0385C, MAL3P3.1.2.
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemos
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z98547; CAB11112.2; HSSP; Q63450; 1A06.
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InterPro; IPR002290; Ser_thr_pkinase.
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Last annotation updat
                                            Score 40; DB Pred. No. 3.1e
1; Mismatches
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SEQUENCE
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Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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01-MAR-2003
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Takami H., Takaki Y., Uchiyama I.;
Takama H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
2-keto-3-deoxygluconate kinase (EC 2.7.1.45)
                                                                                                                                                                                                                                   to the human gastrointestinal tract."; Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002) EMBL; AE014712; AAN24720.1; -.
                                                                                                                                                                                                                                                                                                                           Pridmore R.D., Arigoni
                                                                                                                                                                                                                                                                                                                                Schell M.A., Karmirantzou M., Sne
Pessi G., Zwahlen M.-C., Desiere
Pridmore R.D., Arigoni F.;
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SEQUENCE 320 AA; 35224 MW; 264E9D41C54C09FE CRC64;
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EMBL; AP004600; BAC14169.1; -.
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STRAIN=HTE831 / DS
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MEDLINE=22294977; PubMed=12381787;
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Pred. No. 1.1e+02;
1; Mismatches 1;
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., Bork P., Delley
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                                                                                                        SEQUENCE FROM N.A.

(C) STRAIN=C2A / ATCC 35395 / DSM 2834;

(S) STRAIN=C2A / ATCC 35395 / DSM 2834;

(S) STRAIN=C2A / ATCC 35395 / DSM 2834;

(M) ADLINES=21929760; PubMed=11932238;

(A) Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

(A) FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

(A) FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

(A) Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

(A) Allen N., Naylor J., Stange-Thomann N., DeArellano D.A., Ye W.,

(A) A Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

(A) A Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

(A) A Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

(A) A Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

(A) A Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

(A) A Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

(A) A Pritchet M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

(A) McCall W.W., Birren B.,

(B) McCall W.W., Birren B.,
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                                         and physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8TJS7;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8TJS7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
PF10_0373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 419:498-511(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22255705; PubMed=12368864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003
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                                                                           genome of Methanosarcina acetivorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        surface
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85.7%;
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Apicomplexa; Haemosporida; Plasmodium
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Pred. No. 2.6e
0; Mismatches
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Last sequence up
Last annotation
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annotation update)
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RESULT 12
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Best Local S
Matches
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Best Local S
Matches 6
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01-MAR-2001
01-MAR-2001
                       01-MAR 2001 (TrEMBLrel. 16, Created)
01-MAR 2001 (TrEMBLrel. 16, Last sequence up
01-MAR 2003 (TrEMBLrel. 23, Last annotation
Similarity to polyadenylate-binding protein
Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2001) to the EMBL; AF324983; AAG40335.1; HSSP; P11940; 1CVJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AT5G54900/MBGB_17.

Arabidopsis thallana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; spermatophyta; Magnoliophyta; eudicoceae; Arabidopsis.
    Eukaryota; Viridiplantae;
                                                                                                                                         Q9FFU0;
                                                                                                                                                            Q9FFU0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00076; rrm; 3. SMART; SM00360; RRM; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shinn P., Chao Q.,
Khan S., Kim C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00089; PKD; 7.
PROSITE; PS00018; EF HAND;
PROSITE; PS50093; PKD; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50102; RRM; 3.

PROSITE; PS00030; RRM RNP 1; 1.

SEQUENCE 387 AA; 42324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Arabidopsis cDNA clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Southwick A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miranda M., Nguyen M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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InterPro;
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SEQUENCE 1881 AF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                           372
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                                                                                                                                                                                                                                                                                                                                                               Similarity 6; Conserv
                                                                                                                                                                                                                                                                              YYGGYTGY 379
                                                                                                                                                                                                                                                                                                                     YYGDYEGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chao Q., Brooks S., Chen H., Cheuk R., Johnson-Hopson Kim C.J., Banh J., Bowser L., Chung M.K., Goldsmith M.D. Karrlin-Neumann G., Lam B., Lee J.M., Lin J., Liu S.X., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano A., Toriumi M., Yamada K., Yu G., Davis R.W., Theologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002048; EF-hand.
IPR000413; Integrin_alpha.
IPR000601; PKD_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1881 AA;
                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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75.0%;
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Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               Score 38; DB
Pred. No. 1.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
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Pred. No.
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          D6CF4F66DFD78DB0
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                                                                                        sequence update)
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                                                                                                                                                                                                                                                                                                                                                           1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
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1;
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RESULT 14
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067245;
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InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 2.
Hypothetical protein; Complete proteome.
SEQUENCE 595 AA; 71080 MW; P8373F5603427F24 CRC64;
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Pfam; PF00076; rrm; 3.
SMART; SM00360; RRM; 3.
PROSITE; PS50102; RRM; 3.
PROSITE; PS00030; RRM RNP 1; 1.
SEQUENCE 390 AA; 42652 MW; DD
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Bacteria; Aquificae;
NCBI_TaxID=63363;
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Sato S., Kotani H., Nakamura Y., Kaneko T., F
Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana
"Structural thalysis of Arabidopsis thaliana
features of the 1.6 Mb regions covered by twe
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NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 392:353-358(1998).
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RESULT 15
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                                                                                        "Complete genome sequence of Pseudonoas aeruginosa phage Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY078382; AAL85549.1; -. SEQUENCE 68 AA; 7787 MW; D292B2B7E6EB0E41 CRC64;
                                                                                                                                                                                   Pseudomonas aeruginosa phage PaP3.
Viruses, dsDNA viruses, no RNA sta
T7-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the murine respiratory Mycoplasma pulmonis.";
Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
EMBL; AL445563; CACC13384.1; -.
MypuList; MYPU 2110; -.
MypuList; MYPU 2110; -.
Mypothetical protein; Complete proteome.
SEQUENCE 3216 AA; 359419 MW; A62ED95756BDB90C CRC64;
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MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., S:
Moszer I., Dybvig K., Wroblewski H., Viari A.,
Blanchard A.;
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Bacteria; Firmicutes;
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Hypothetical protein MYPU_2110.
MYPU_2110.
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
SUMMARIES
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ALIGNMENTS

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(IMCL-) IMCLONE SYSTEMS INC.	29-JAN-1999; 99US-0240736.	29-JAN-1999; 99US-0117726.	28-JAN-2000; 2000WO-US02180.	CO BOO BOOC.	03-1170-2000	WO200044777-A1.		nound sapreis.		acquired immune deficiency syndrome; AIDS; human.	central nervous system neoplasms; AIDS associated Karposi's sarcoma;	glioblastoma multiforme; hemangioblastoma; AIDS;	humanised antibody; chimeric antibody; tumour; diabody; triabody;	kinase insert domain containing receptor; multivalent; monovalent;	VEGF; vascular endothelial growth factor; KDR;	Immunoglobulin; antibody; complementary determing region; CDR;		Complementary determining region (CDRH3) of anti-SI(KDR) antibody.	19-DEC-2000 (first entry)		AA19/231;		AAY97231 standard; Protein; 8 AA.	RESULT 1 AAY97231

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RESULT 2
AAE13139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VBGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single chain antibody, a diabody, a diabody or a chimerised antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as the extracellular domain of the KDR receptor with the same affinity as extracellular domain of VBGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the
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Best Local (
                                                                                                                                                                                                                                                                                          Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; heavy chain hypervariable region; VH; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.
                                      WPI; 2001-662942/76.
N-PSDB; AAD21665.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; peptide; 8 AA
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                                                                                Rafii
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                                                                                                            FOUND INC
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Pred.
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9.3e+05;
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Inhibiting frowth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with

Disclosure; Page 37; 42pp; English

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RESULT 3
AAB82705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      involves treating the mammals with humanised Vascular endpitchelial involves treating the mammals with humanised VEGFR monoclonal mattibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those relaited to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody murine heavy chain hypervariable region (VH) CDR-3 used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                       Chimeric -
Chimeric -
                         chemotherapeutic agent
                                         administering
                                                                                                                                                                                                                28-JAN-2000;
31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  colon carcinoma; ovarian carcinoma; neuroblastoma;
glioblastoma multiforme; melanoma; therapy; heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGF antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method
                                                                                                      WPI; 2001-514531/56.
                                                                                                                                                                                                                                                                                             02-AUG-2001
                                                                                                                                                                                                                                                                                                                        WO200154723-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB82705 standard;
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                                                                                                                                                                                                                                                             29-JAN-2001; 2001WO-US02839
                                                                                                                                                                                                                                                                                                                                                                                                   complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour; breast carcinoma; lung carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB82705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an antagonist of a vascular endothelial growth factor receptor
                                                                                                                                                                   (IMCL-)
                                                                                                                                                                                   SUNN-)
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                                                                                                                                                                   IMCLONE SYSTEMS INC
                                                                                                                                                                                 SUNNYBROOK HEALTH SCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                        or controlling an angiogenic dependent condition (e.g., collagen-vascular or autoimmune disease) in mammal by ering a combination of an antiangiogenic molecule and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YYGDYEGY
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                                                                                                                                                                                                                2000US-0178791.
2000US-0539692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                   determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody IMC-1C11 VH CDR-3.
                                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide; 8
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                                                                                                                                                                                                                                                                                                                                                                                                                melanoma; therapy;
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Pred. No. 9.3
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                  heavy chain;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cor a fragment of it, can be used as an anti-anglogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, sepecially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a cascular endothelium survival factor such as VEGF or its receptor, and is especially INC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, call claimed).
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Best Local :
                                                       Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparathuman vascular endothelial growth factor, and neutralizes activat
                                                                                                                             N-PSDB;
                                                                                                                                            WPI; 2002-589175/63.
                                                                                                                                                                                                                                                        28-JAN-2000; 2000US-0493539
                                                                                                                                                                                                                                                                                                                          30-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR; foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor; VEGF; tumour growth; heavy chain complementarity determining region 3; CDRH3; angiogenesis; plCl1; scFv antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse anti-KDR p1C11 scFv antibody CDRH3 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-NOV-2002 (first entry)
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                                                                                                                                                                           Zhu Z,
                                                                                                                                                                                                            (XTTY)
                                                                                                                                                                                                                                                                                         12-OCT-2001; 2001US-0976787.
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8; Conservative
                                                                                                                             AAD42816.
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Pred. No.
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ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The antibody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                            comparable activation
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Claim 3;

Page 11; 34pp; English

in the desired configuration.

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FIK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR plC11 scFv antibody heavy chain complementarity determining region 3 (CDRH3) protein.
             (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting VEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled substantially all of the antigen-binding proteins produced.
                                                                                                                                              The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                        New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-106189/14.
N-PSDB; AAS20279.
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                                                                                                                                                                                                                                                                                                      Claim 55; Page 56; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhu Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-2001; 2001WO-US16924.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis inhibitor; vascular endothelial growth for
VEGF; tumour; leukaemia; antibody; cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity determining region; CDR; CDRH3; antigen; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMCL-) IMCLONE SYSTEMS INC
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8; Conserv
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Pred. No. 9.3e+05;
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bispecific,
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RESULT 6
ABJ26720
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Best Local S
Matches 8
                                Query Match
Best Local Similarity
Matches 8; Conser
                                                                                              Sequence
                                                                                                                                                                     The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGP) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; mouse; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This peptide sequence represents the heavy chain variable domain complementarity determining region H3 (CDRH3) incorporated into an antigen-binding protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                           New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia
                                                                                                                             methods. This sequence represents a mouse peptide relating to-
bispecific antibodies that bind to the VEGF receptors of the i
                                                                                                                                           tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a money possible and diagnostic
                                                                                                                                                                                                                                                                                              Claim 6; Page 48; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-201468/19.
N-PSDB; ABT23298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF binding related peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001; 2001US-301299P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2002; 2002WO-US20332
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8; Conserv
                                                                                                                                                                                                                                                                                                                          for treating tumors -
100.0%;
Lity 100.0%;
Conservative
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                                Score 51; DB Pred. No. 9.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51;
Pred. No.
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                                 9.3e+05;
hes 0;
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                                                                DB 24;
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                                                                                                                           receptors
                                                            Length 8;
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                                 Gaps
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RESULT 7
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                                                                                                New immunoglobulin molecules are described that bind kinase insert C domain-containing receptor (KDR) with a comparable affinity to human C vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single C chain antibody, a monovalent single chain antibody, a diabody, a criabody, a humanised antibody or a chimerised antibody. The immunoglobulin molecules bind specifically to an C triabody, a humanised antibody or a chimerised antibody as C C vEGF. Overexpression of the KDR receptor with the same affinity as C vEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, humanisoblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the
                Query Match
                                                   Sequence
                                                                                    preferred heavy chain complementary immunoglobulins of the invention.
                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 50-51; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  used to
                                                                                                                                                                                                                                                                                                                                                                                                                Novel immunoglobulin molecules binding kinase insert domain-correceptor with the same affinity as vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-1999;
29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               humanised antibody; chimeric antibody; tumour; diabody; triabody; glioblastoma multiforme; hemangioblastoma; AIDS; central nervous system neoplasms; AIDS associated Karposi's sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-2000; 2000WO-US02180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acquired immune deficiency syndrome; AIDS; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variable heavy chain fragment of anti-SI(KDR) antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY97235 standard; Protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMCL-) IMCLONE SYSTEMS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEGF; vascular endothelial growth factor; KDR; kinase insert domain containing receptor; multivalent; monovalent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin; antibody; complementary determing region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-505966/45.
                                                                                                                                                                                                                                                                                                                                                                                                reduce tumour growth
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                                                   117 AA;
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99US-0240736.
100.0%;
 Score 51; DB 2
Pred. No. 0.63;
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                DB 21;
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YYGDYEGY 106

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RESULT 8
RESULT 9
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                                                                                                                                                Matches
                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                              The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic lymphocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody heavy chain frgament used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised antibody heavy chain fragment
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               AAB82709 standard; Protein; 117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              numan;
                                                                                                                                                              Local Similarity
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CORNELL RES FOUND II
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                                                                                        YYGDYEGY 106
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                                                                                                                                                Conservative
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                                                                                                                                                              100.0%;
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                                                                                                                                                              Score 51;
Pred. No.
                                                                                                                                                Mismatches
                                                                                                                                                            0.63;
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X P A X R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Χ̈́В
                                                                         angiogenic dependent condition in a mammal, especially a human.
The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent.
The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-IC11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, cespecially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma, system tumour, including account of the carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma, system tumour, and the carcinoma, colon carcinoma, system tumour, colon carcinoma, prostate carcinoma, colon carcino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514531/56.
N-PSDB; AAH26405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vascular endothelial growth factor; angiogenesis; antiangiogenic;
antitumour; neoplasm; collagen-vascular disease; autoimmune disea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of the heavy chain variable region of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating or controlling an angiogenic dependent condition neoplasm, collagen-vascular or autoimmune disease) in mamm administering a combination of an antiangiogenic molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-2000; 2000US-0178791.
31-MAR-2000; 2000US-0539692.
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colon carcinoma; ovarian carcinoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEGF antagonist antibody IMC-1C11 heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemotherapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kerbel R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2001; 2001WO-US02839.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200154723-A1
                                                         neuroblastoma, glioblastoma multiforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMCL-) IMCLONE SYSTEMS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CDR-H2
/note= "complementarity determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= CDR-H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= CDR-H1
                                                            or melanoma
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                                                            claimed)
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Sequence

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AAE25955
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          AAU74412 standard; peptide; 117 AA
                                                                                                                                                                                          to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGP) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR plCl1 scFv antibody heavy chain variable region (VH).
                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                       Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-589175/63.
N-PSDB; AAD42820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR; foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor; VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;
                                                                                                                                                                                                                                                                               The present
                                                                                                                                                                                                                                                                                                      Claim 4; Page 11; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              Zhu Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-2000; 2000US-0493539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse anti-KDR p1C11 scFv antibody VH region #1.
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                                                                                             1 YYGDYEGY 8
                                                                                                                    8; Conserv
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WITTE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scrv antibody
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8; Conser
                                                                       YYGDYEGY 106
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                                                                                                                                                                    117
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                              invention relates to novel immunoglobulin molecules that bind
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Pred. No.
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Pred. No. 0.63;
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                                                                                                                                0.63;
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RESULT 12 AAU74417 ID AAU74 XX

AAU74417 standard; peptide; 117

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8
                                                                                                                Matches
                                                         Query Match
Best Local :
                                                                                                                                                migration of human leukaemia cells; blocking interaction of approtein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain (VH) incorporated into Fv, an engineered protein containing a heavy chain variable domain and a light chain variable domain in one polypeptide chain, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an antigen-binding protein (I) compriging a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor, reducing tumour growth, inhibiting unglogenesis, reducing endothelial cell proliferation, inhibiting VEGF induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
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                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-106189/14.
N-PSDB; AAS20283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 57; Page 57; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-2000; 2000US-206749P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-2001; 2001WO-US16924.
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                                                                                                                117 AA;
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                                                       100.0%;
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                                                         Score 51; DB 2:
Pred. No. 0.63;
                                     Mismatches
                                                                           DB 23;
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                                                                           Length 117;
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AAU74417;

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RESULT 13
ABJ26724
ID ABJ26
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                                                                                                                                                                                                                                                       CC complex of two polypeptides (P1) and two second polypeptides (P2) which CC complex of two polypeptides (P1) and two second polypeptides (P2) which CC are stably associated in an immunoglobulin like complex. P1 has an CC antigen-binding site located to the N terminus of immunoglobulin (Ig) CC light chain constant domain (CL domain), and P2 has an antigen-binding CC site located to the N terminus of the CH1 domain. (I) is useful for: CC (NEGF) receptor; reducing tumour growth; inhibiting angiogenesis; CC reducing endothelial cell proliferation; inhibiting ungiogenesis; CC reducing endothelial cell proliferation; inhibiting ungiogenesis; CC and in vivo and in vitro for investigative, diagnostic or treatment CC methods. The design of (I) provides for efficient production so that CC in the desired configuration. (I) is bivalent and bispecific, homogeneous CC and in tetrameric form. The heavy chain constant domains which constitute CC antibody and which provides other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain (VH) incorporated contain variable domain in one polypeptide chain, described in CC the method of the invention.
                                                                                                                                                             Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides -
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               ABJ26724 standard; Protein; 117 AA.
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 61; Page 60; 64pp; English.
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                                                                                               YYGDYEGY 106
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                                                                                                                                                              Conservative
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Pred. No.
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; antibody; antigen binding site; VEGF receptor; leukaemia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; mouse; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New bispecific antibodies having antigen-binding sites specific for first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells, or for treating tumors -
                                                     bispecific
                                                                Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour;
                                                                                                           VEGF binding related
                                                                                                                                       01-MAY-2003
                                                                                                                                                                                               ABJ26729 standard; Protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 49;
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8; Conserv
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                                                                                                                                                                                                                                                                   YYGDYEGY 106
                                                   antigen-binding protein; mouse; murine.
                                                                                                                                                                                                                                                                                                                                                                                  117 AA;
                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                           protein
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Pred. No. 0.6
0; Mismatches
                                                                                                           SEQ ID
                                                                                                             No
                                                                                                             22.
                                                                                                                                                                                                                                                                                                                                       0.63;
                                                                                                                                                                                                                                                                                                                                                   DB 24;
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                                                                                                                                                                                                                                                                                                                                                      Length 117;
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WO2003002144-A1

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RESULT 15
AAE25965
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Best Local Similarity
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                    Mouse;
foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells,
                         Region
                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                         p1C11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-2003
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DB; ABT23307.
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                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin; kinase insert domain-containing receptor; KDR;
liver kinase; FLK-1 receptor; vascular endothelial growth fact
tumour growth; heavy chain variable region; VH; anglogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              p1C11 scFv antibody VH region #2
                    /note= "Heavy chain complementarity determining region 2 (CDR-H2)" 118..125
                                                                                  /note= "Heavy chain complementarity determining region 1 (CDR-H1)"
                                                                                                                                                       /note= "Mouse p1C11 scFv antibody mature 45..54
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                  /label= Signal-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
"Heavy chain complementarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51; DB 2. Pred. No. 0.63;
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                                                                                                                                                                                                                                                                                                                                                                                                factor;
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Best Local S
Matches 8
                                                                                                                               The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KOR) (a human homologue of mouse foetal liver kinase (FIK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR plCll scFv antibody heavy chain variable region (VH).
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
                                                                                                                                                                                                                                                          Disclosure; Fig 4; 34pp; English
                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD42832
                                                                                                                                                                                                                                                                                                                                                                                                Zhu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-2000; 2000US-0493539
                                                                                                                                                                                                                                                                                                                                                                                                                       (ZHUZ/) ZHU Z.
(WITT/) WITTE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2001; 2001US-0976787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002064528-A1
                                                     Local Similarity
nes 8; Conserv
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  118
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YYGDYEGY 125
                          УУСРУЕСУ 8
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ilarity 100.0%;
Conservative (
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                                                     Score 51; DE
Pred. No. 0.7
0; Mismatches
                                                                  DB 2:
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length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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        Query
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Copyright (c) 1993 - 2003
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/Cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*
/Cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*
/Cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/Cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
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/Cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
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1 US-09-865-198-22
1 US-09-865-198-28
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US-09-798-689-3
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Compugen Ltd
Sequence 3, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 23, Appl
Sequence 22, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 29, Appl
Sequence 28, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 27, Appl
                                                                                                                                                                                                                                                                                                                                                  Description
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APPLICANT: Zhu, Zhenping

APPLICANT: Witte, Larry

TITLE OF INVENTION: Antibodies Specific to KDI

FILE REFERENCE: 11245/46505

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 09/493,539

PRIOR FILING DATE: 2000-01-28

PRIOR PILING DATE: 2000-01-28

PRIOR PILING DATE: US 60/117,726

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 3

LENGTH: 8

TYPE: PRT
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US-09-976-787-3
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Matches 8
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ALIGNMENTS

KDR and Uses Thereof

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RESULT 2
US-09-865-198-3
; Sequence 3, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
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8; Conser
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                                                                                                                     YYGDYEGY
                                                                                                                                                                          100.0%; Score 51; Di
ilarity 100.0%; Pred. No. 4e-
Conservative 0; Mismatches
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                                                      GENERAL INFORMATION:
                                                                     Sequenca 7, Application US/09976787 Patent No. US20020064528A1
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Best Local Similarity
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TITLE OF INVENTION: Method for Reducing Tumo
TITLE OF INVENTION: Combined With Radiation
FILE REFERENCE: Sequence Listings 1-41 for
CÜRRENT APPLICATION NUMBER: US/09/798,689
CÜRRENT FILING DATE: 2001-03-02
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CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
                                    APPLICANT: Zhu,
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER:
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APPLICANT: Goldstein, Neil I.
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PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
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NPPLICANT Witte, Larry TILE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
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                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mouse
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ORGANISM: Mouse
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                                  Zhenping
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Pred. No.
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US-09-976-787-23
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TITLE OF INVENTION: Antibodies Specific to KD
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
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APPLICANT: Zhu, Zhenping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 23
LENGTH: 117
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Best Local
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SOFTWARE: WordPerfect 8.0 for Windows SEQ ID NO 7
                                                      TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Production FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR PILING DATE: 2000-05-24
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                                         NUMBER OF SEQ ID NOS: 34
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
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APPLICANT: Witte, Larry
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TYPE: PRT
ORGANISM: Mus musculus
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8; Conserv
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Pred. No.
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Best Local Similarity
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; ORGANISM: Mouse
US-09-865-198-7
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Best Local Similarity lou.
The B; Conservative
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FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR PILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2 Patent No.
                               SEQ ID NO 7
LENGTH: 117
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Publication No. US2003010397731
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                                                                                                                                                                                                                                                                                                                 APPLICANT: Goldstein, Neil I.

TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
                                                                                                                                                                                                            PRIOR FILING DATE: 1997-PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996-0
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-0
                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/967,113 PRIOR FILING DATE: 1997-11-10
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                                                                                                                                                                            PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1995-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
ORGANISM: Mouse
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                                                                                              APPLICATION NUMBER: 08/
                                                                                                                                           FILING DATE:
                                                                                                                                                          APPLICATION NUMBER: 08/326,552
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                                                                    PatentIn Ver. 2.1
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                                                                                                                        08/196,041
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YYGDYEGY 106

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; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28
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Best Local Similarity
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US-09-865-198-28
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Best Local Similarity
""" hes 8; Conservat
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; ORGANISM: Mouse
US-09-976-787-29
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                                                                                                                                                             NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.
SEQ ID NO 28
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                                   Matches
                                                               Query Match
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                                                Best Local Similarity
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
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Patent No. US20020064528A1
                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho TITLE OF INVENTION: Production FILE REFERENCE: 11245/47102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to
FILE REFERENCE: 11245/46505
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Pred. No. 0.25;
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Pred. No. 0.49;
                                   Mismatches
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                                                                 DB 10;
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SEC ID NO 21
LENGTH: 238
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Patent No.
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                                                                                     Query Match
Best Local Similarity
                                                                                                                                             ORGANISM: Mouse -09-976-787-28
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SEO ID NO 28
LENGTH: 240
TYPE: PRT
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Best Local
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Publication No. US20030103973A1
                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to
FILE REFERENCE: 11245/46505
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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PRIOR APPLICATION NUMBER: 08/9

PRIOR APPLICATION 1997-11-1/
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CURRENT FILING DATE: 2001-03-02
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FILING DATE: 1994-02-10
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5. US20020064528A1
99 YYGDYEGY 106
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8; Conserv
                                   YYGDYEGY 8
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                                                                       Conservative
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Sequence Listings 1-41 for
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100.0%; Pred. No.
                                                                    100.0%; Score 51; DB 9;
100.0%; Pred. No. 0.5;
cive 0; Mismatches 0
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                                                                                                       Length 240;
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; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27
                                                                                              RESULT 15
US-10-156-761-9497
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US-09-821-687-11
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APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR PILING DATE: 2000-05-24
                                                         Sequence 9497, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                    72.5%;
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MIKOSHIBA, KATSUHIKO
APPLICANT: MIZUTANI, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: W
SEQ ID NO 27
                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Patent No. US20020103345A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09821687 Patent No. US20020106724A1
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: RNA-BINDING PROTEIN FILE REFERENCE: 081356/0162 CURRENT APPLICATION NUMBER: US/09/821,687 CURRENT FILING DATE: 2001-07-03
                       APPLICANT: OMURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2000-299812 PRIOR FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 335
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Unknown Organism: m-hnRNPR
                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Unknown Organism
                                                                                                                                                                           172 YYDDYYGY 179
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                     , SATOSHI
HARUO
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51; DB 10;
Pred. No. 0.5;
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APPLICANT:

ISHIKAWA, JUN HORIKAWA, HIROSHI SHIBA, TADAYOSHI

SAKAKI,

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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9497
LENGTH: 522
TYPE: PRT
CORGANISM: Streptomyces avermitilis
US-10-156-761-9497

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
Search completed: July 30, 2003, 10:20:28

Search completed: July 30, 2003, 10:20:28
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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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51
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131.295 Million cell updates/sec
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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           US-08-888-366-12

US-09-136-315-2

US-09-136-315-2

US-09-136-315-2

US-09-252-991A-27051

US-09-38-352-4356

US-09-134-001C-3350

US-09-107-532A-6201

US-07-857-224B-61

US-07-857-224B-61

US-08-467-580-42

PCT-US95-08516-42

PCT-US95-08516-42

US-09-252-991A-32408

US-09-252-714-28

US-09-328-352-7577

US-08-225-477B-8
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PCT-US95-08516-43
US-09-113-750A-35
US-09-134-078-61
US-09-134-078-25
US-08-313-200-1
US-08-313-200-1
US-09-251-039-2
PCT-US93-03837-1
US-09-646-028-13
US-09-646-028-15
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                      Sequence
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e 25, Appl
i 2, Appli
i 1, Appli
i 1, Appli
i 16, Appl
i 13, Appl
i 13, Appl
i 15, Appl
                                             61, Appl
42, Appl
42, Appl
32408, A
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2, Appli
6, Appli
6, Appli
27051, A
27051, A
356, Ap
3350, Ap
6201, Ap
28, Appl
5757, Ap
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US-08-467-580-43
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64.7	64.7	64.7	64.7	64.7	64.7		64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7
485	485	485	485	485	485	485	485	485	485	485	485	485	485	405	402	400	389
W	ω	ω	w	ω	w	w	w	ω	N	N	N	N	N	4	4	w	4.
US-09-170-670-8	US-09-170-670-7	US-09-170-670-6	US-09-170-670-2	US-09-170-670-1		US-08-600-656-2	US-08-600-656-1	US-08-683-838A-12	US-08-600-908A-12	US-08-861-837-2	US-08-861-837-1	US-08-446-803-2	US-08-446-803-1	US-09-291-023A-20	US-09-055-765-14	US-09-264-097-6	US-09-055-765-13
e 8	e 7,	Sequence 6, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 12, Appl	12,	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 20, Appl	Sequence 14, Appl	Sequence 6, Appli	Sequence 13, Appl

ALIGNMENTS

```
APPLICANT: Thorsett, Eugene D
APPLICANT: Yednock, Theodore A
APPLICANT: Yednock, Theodore A
APPLICANT: Pleiss, Michael A
TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
FILE REFERENCE: 123-US-CIP1
CURRENT APPLICATION NUMBER: US/08/467,580B
CURRENT FILLING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/273,055
EARLIER FILLING DATE: 1994-07-11
NUMBER OF SEQ ID NOS: 163
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 43
LENGTH: 11
                                                                                                PCT-US95-08516-43
PCT-US95-08516-43
; Sequence 43, Application PC/TUS9508516
; GENERAL INFORMATION:
; APPLICANT: ATTION: INFORMATION: INC.
TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
; NUMBER OF SEQUENCES: 157
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD RES
LOCATION: (1)
OTHER INFORMATION:
US-08-467-580-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43, Application US/08467580B Patent No. 6001809
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                CORRESPONDENCE ADDRESS
ADDRESSEE: ATHENA NI
STATE: CA
                                                                                                                                                                                                                                                                                                        1 YYGDYEGY 8
                                                                                                                                                                                                                                                                     YYGNYGGY 10
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description of Artificial Sequence: Peptide derived from VCAM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLATION
                                                                                                                                                                                                                                                                                                                                                           76.5%;
75.0%;
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Pred. No. 2
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No. 6294176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5574
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)262-0400
TELEPAX: (212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEPAX: (415) 877-3620
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,055
FILING DATE: 11.JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: MODI, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 002010-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-BC868 #1.0, VC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08516
FILING DATE: 10-UUL-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: .David E. TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                            CLASSIFICATION: 424
                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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ENGTH:
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                                                     422523
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                                                                                                                                                                                                                                                                                                                                                                                                                             B: John P. White
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Junker and Mark D. Cochran Recombinant Raccoonpox virus
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Pred. No. 2.2;
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                                                                                                               ; TYPE: amino acid
TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-134-078-61
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                                                       Matches
                                                                      Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                       FILING DATE: 13-AUG-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/949,02
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,91
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                    TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bylina, TITLE OF INVENTION:
                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
 361
                           1 YYGDYEGY 8
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YYPDYDGF 368
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                                                                                                                                                                                     663 amino acids
                                                                                                                                                                                                                                 858/677-1456
858/677-1465
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                                                       Conservative
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                                                                      70.6%;
62.5%;
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GLYCOSIDASE ENZYMES
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75.0%;
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Pred. No. 2
                                                                      Score 36; DB 4; Pred. No. 3.4e+02;
                                                         Mismatches
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                                                         1; Indels
                                                                                    Length 663;
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                                                       Gaps
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RESULT 5 US-09-134-078-25 ; Sequence 25, Application US/09134078 ; Patent No. 6368844

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Query Match
Best Local Similarity 6
Watches 5; Conservati
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                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08313200
Patent No. 5998153
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL, INFORMATION:
APPLICANT: Bylina,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO:
             ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                    STREET: /50
CITY: Palo Alto
CTATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 680 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/134,078
                                                                                                                                                                                                          NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSEE: MORRISON & FOERSTER
ADDRESSEE: 755 Page Mill Road
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                     APPLICANT: Baker, James R. APPLICANT: Koenig, Ronald J. TITLE OF INVENTION: THYROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4365 Exe
CITY: San Diego
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: Windows95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0:
FILING DATE: 13-AUG-1998
                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 YYPDYDGF 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YYGDYEGY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.6%;
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US/08/313,200
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Pred. No. 3.5e+02;
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LOCATION: 376..631
OTHER INFORMATION: /
OTHER INFORMATION: fi
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: Region
LOCATION: 266..281
OTHER INFORMATION: /
OTHER INFORMATION: /
FEATURE:
                                                                      NAME/KEY: Region
LOCATION: Join (455..532, 590..933)
OTHER INFORMATION: /note= "alternatively spliced OTHER INFORMATION: C-terminus of TPO"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, AUTOINETE F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
LOCATION: join(1..3, 456..631)
OTHER INFORMATION: /note= "TPO region within fusion
OTHER INFORMATION: plasmid: TPO(delta4-455)"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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NAME/KEY: Region
LOCATION: 455..933
OTHER INFORMATION: /
OTHER INFORMATION: b
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide LOCATION: 1..631 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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LOCATION: 1..400
OTHER INFORMATION:
OTHER INFORMATION:
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706141
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TISSUE TYPE: Thyroid gland(from people with Grave's
TISSUE TYPE: disease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: phTPO-2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 933 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 813-5600
                                                                                                                                                                                                                                                                        region"
   /note= "TPO C-terminus containing
binding region"
                                                                                                                                                                                /note= "TPO epitopic region within
fusion protein: MBP-TPO (AA 376-631)"
                                                                                                                                                                                                                                                                                                                                                                     /note= "C-terminal truncation:
TPO(1-631)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "C-terminal truncation-
TPO(1-455) or N-terminal half of TPO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "C-terminal truncation:
TPO(1-120)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "TPO epitopic region within fusion protein: MBP-TPO (AA 1-400)"
                                                                                                                                                                                                                                                                                             /note= "TPO epitopic or binding
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NAME/KEY: Region
LOCATION: 457..517
OTHER INFORMATION:
FEATURE:
NAME/KEY: Region
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NAME/KEY: Region
LOCATION: 517..630
OTHER INFORMATION: /
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NAME/KEY:
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NAME/KEY:
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LOCATION: 465..933
OTHER INFORMATION:
OTHER INFORMATION:
                                                                    NAME/KEY: Region
LOCATION: 590..615
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                      NAME/KEY: Region
LOCATION: 590..611
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 573..633
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 517..633
OTHER INFORMATION:
OTHER INFORMATION:
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NAME/KEY:
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LOCATION: 457..633
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 456..933
OTHER INFORMATION: OTHER INFORMATION: 1
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LOCATION: 456..933
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 456..633
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
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LOCATION:
NAME/KEY: Binding-site LOCATION: 590..675
OTHER INFORMATION: /not OTHER INFORMATION: regi
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LOCATION:
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TION: 457..933
R INFORMATION:
R INFORMATION:
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513..633
                                                                 /note= 'region"
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region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "maltose
/note= "TPO binding or epitopic
region"
                                                                                                                                                                                                                                                                          /note= "TPO
region"
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                                                                                                                                   /note= "TPO region within maltose binding fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "TPO binding region within plasmid pMalTPO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "TPO region within fusion
plasmid pMalTPO"
                                                                                                                                                                                                                                                                                                                                                region"
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binding fusion protein"
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                                                                                 "TPO
                                                                                                                                                                                                                                                                                                                                                               OdI.
                                                                                                                                                                                                                                                                                                                                                                                                                  "recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "TPO binding region of binding region fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "TPO
                                                                                                                                                                                                                     "TPO binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "non-reactive fragment"
                                                                              binding
                                                                                                                                                                                                                                                                                        binding
                                                                                                                                                                                                                                                                                                                                                            binding
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; TYPE: PRT
; ORGANISM: Homo
US-09-251-039-2
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US-09-251-039-2
                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/251,039
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/313,200
EARLIER FILING DATE: 1994-11-08
EARLIER APPLICATION NUMBER: 07/885,656
EARLIER FILING DATE: 1992-05-19
EARLIER APPLICATION NUMBER: PCT/US93/03837
EARLIER FILING DATE: 1993-04-22
Query Match
Best Local Similarity /ɔ..
Conservative
                                                                                                                                                   SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 596..611
OTHER INFORMATION: /
OTHER INFORMATION: PEATURE:
                                                                                                                                                                  NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, James R.
APPLICANT: Koeniq, Ronald J.
APPLICANT: University of Michigan
TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC
FILE REFERENCE: 203442065801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Region
LOCATION: 592.613
OTHER INFORMATION: /
FEATURE:
FEATURE:
                                                                                                                                   ENGTH: 933
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LOCATION: 632..933
OTHER INFORMATION: /
OTHER INFORMATION: 1
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LOCATION: 631..933
OTHER INFORMATION: 0THER INFORMATION: 1
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LOCATION: 611..615
OTHER INFORMATION: 0THER INFORMATION: 1
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LOCATION: 602..615
OTHER INFORMATION: OTHER INFORMATION:
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LOCATION: 633..768
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 YVGPYEGY 473
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                                                                                                     sapiens
                                     70.6%;
75.0%;
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75.0%;
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binding fusion protein"
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protein"
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region"
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                     Score 36; DB 4; Luc
Pred. No. 4.7e+02;
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Pred. No. 4.7e+02;
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                                                    Length 933;
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466 YVGPYEGY 473

YYGDYEGY

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Query Match
Best Local Similarity
Thes 6; Conserve
                                                                       DATE: 1987
RELEVANT RESIDUES IN SEQ ID NO:
PCT-US93-03837-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 641-1600
TELEPAX: (313) 641-0270
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N
ORIGINAL SOURCE:
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1in
MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baker, Jr., James R.
APPLICANT: Koenig, Ronald J.
TITLE OF INVENTION: Thyroid Peroxidase Epitopic Regions
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 933 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Lewak, Anna M.
REGISTRATION NUMBER: 330
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: Mature TISSUE TYPE: Thyroid gland (from people with Grave's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: P.O. Box 828
CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 199304
                                                                                                                                                          TITLE: protein sequence, chromosome mapping, and TITLE: identification of two alternately spliced mRNAs JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                             AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                            5555-5559
                                                                                                                                                                                                         Human thyroid peroxidase:
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Umeki, K.
Nakayama, T.
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Kotani, T.
McBride, O. W.
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Hirai, K.
               Conservative
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                             70.6%;
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             Score 36; DB 5;
Pred. No. 4.7e+02;
0; Mismatches 2
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                                                                                                                                                                                                           Complete cDNA and
                                                                                              FROM 1 TO 3048
                                          Length 933;
               Indels
             0
             Gaps
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Sequence 13, Application:

Bequence 13, Application:

Patent No. 6562347

BERNAL INFORMATION:

APPLICANT: Kwak, Larry

APPLICANT: Biragyn, Arya

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION

TO DEFERENCE: 14014.0316/P

TO DEFERENCE: 14014.0316/P
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                                                                                                                                  ; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct US-09-646-028-13
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                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ for
SEQ ID NO 13
LENGTH: 361
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-646-028-13
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Matches
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SOFTWARE: FastSEQ for
SEQ ID NO 16
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APPLICANT: Kwak, L
APPLICANT: Biragyn
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                                                                  Matches
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                                                                                  Query Match
Best Local Similarity
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CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KWAA, WALLY
APPLICANT: Biragyn, Arya
ATYA
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 359
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les 6; Conserv
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196 YDGSYEGY 203
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                                1 YYGDYEGY 8
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BER: 60/077,745
                                                                                  68.6%;
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                                                                                  Score 35; I
Pred. No. 2
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Pred. No. 2.7e+02;
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                                                                  Mismatches
                                                                                  DB 4;
2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                               FUSION PROTEINS AS CANCER VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUSION PROTEINS AS CANCER VACCINES
                                                                                                Length 361;
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                                                                    Indels
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RESULT 11 US-09-646-028-15

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RESULT 12
5268270-2
;Patent No.
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Best Local Similarity
Watches 6; Conserv
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; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Meyer, Thomas F.;Halter, Roman;Pohlner, Johnnnes
TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM
NEGATIVE HOST CELLS
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/171,872
FILING DATE: 01-JUL-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 15
                                                                                                                                                                                                                                                    Patent No. 5972656
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                             APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercur
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                            NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
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                                        COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1507
                                                                                                                             ADDRESSEE:
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                                                                                          Minneapolis
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                                                                           3
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                                                                                                           8: Merchant & Gould
90 South 7th Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kwak, Larry
                                                         USA
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Pred. No. 1.1e+03;
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Pred. No. 2.8e+02;
                                                                                                           3100 No. 5972656west Ctr
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Best Local Similarity 64...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                      Matches
                                                                                                                                                                         Query Match
Best Local
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Patent No. 6228360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILLIANO
TITLE OF INVENTION: ANTITHROMBOTIC AGENT AN
TITLE OF INVENTION: FACTOR MONOCLONAL ANTIF
FILE REFERENCE: 0010-0933-0
CURRENT APPLICATION NUMBER: US/09/136,315B
CURRENT FILING DATE: 1998-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                        LENGTH: 139
TYPE: PRT
ORGANISM: Mus musculus
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Carter C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/187,407
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
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                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Carter, Charles G. REGISTRATION NUMBER: 35,
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Pred. No. 1.5e+02;
1; Mismatches 2;
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US-09-13-3-15-6

Sequence: 6, Application US/09136315B;
Patent No. 6228360

GENERAL INFORMATION:
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILLIANO
TITLE OF INVENTION: ANTIFROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
TITLE OF INVENTION: PACTOR MONOCLONAL ANTIBODY
TILE OF INVENTION NUMBER: US/09/136,315B
CURRENT FILING DATE: 1998-08-19
CURRENT FILING DATE: 1998-08-19
INVHER OF SEO ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
SEQ ID NO
SEQ ID NO
SEQ ID NO
DEGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-136-315-6

Query Match
Best Local Similarity 62.5*; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
DB 119 YYGSYGGF 126

Search completed: July 30, 2003, 09:38:28

Job time: 3.57807 secs
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Match
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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CDR1 from light chain CDR1 of light chain Peptide fragment for Complementary determine the Anti-human VEGF resumanized antibody VEGF antagonist an Mouse ganglioside
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ALIGNMENTS

RESULT 1 AAW27424

AAW27424;

19-DEC-1997 (first entry)

CDR1 from light chain variable region of KM1486 antibody.

AAW27424 standard; peptide; 10

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Complementarity determining region; CDR; light chain; treatment; variable region; murine; mouse; human; interleukin 5; II-5; receptor; alpha chain; monoclonal antibody; hybridoma; detection; assay; diagnosis; allergic respiratory disease; chronic bronchitis; Anazawa H, Nakamura K, Mus WPI; 1997-202249/18 11-SEP-1995; 11-SEP-1996; 20-MAR-1997. W09710354-A1. (КУОМ) КУОМА НАККО КОБУО КК spp. Furuya A, Takatsu K 95JP-0232384. 96WO-JP02588. ζ, Hanai N, Iida A, Koike M;

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Best Local S
Matches 10
                                                                                           This sequence represents a complementarity determining region (CDR) from the heavy chain of the antibody of the invention. The antibody of the invention is a human CDR transplanted antibody that reacts specifically with ganglioside GM2. DNA encoding the antibody, and vectors and transformants containing it, can be used for the recombinant production of the antibody. The antibody itself can be used as an anti-tumour agent or as a diagnostic tool for related cancers. The antibody has antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A human type complementarity determining region transplanted antibody against ganglioside GM2 - useful as an anti-tumour agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ganglioside GM2; antibody; complementarity determining region; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 29; 66pp; Japanese.
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                                                                                                                                                              Sequence
                                                                                                                                                                                                                        Chimeric human antibodies of the invention are useful in the treat of cancer, especially that which is of neural ectodermal origin. In contrast to prior art constructs based on mouse monoclonal antibodies, the chimeric human antibodies do not cause anti-mouse
                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
07-SEP-1993;
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                                                                                                                                                                                                      The chimeric
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                                                                                                                                                                                                               mmunoglobulin production
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ilarity 100.0%;
Conservative 0
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93US-0116778.
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                                                                                                                      Score 48; DB 20;
Pred. No. 0.0063;
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Pred. No. 0.0063;
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                                                                                                                                                                                                                                                                          the CDR regions of the NEWM human anti-GM2 antibody lig
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RESULT 5
AAY77582
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                                                                                                                                                                                                                                                                                                                                                  New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (YBGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single chain antibody, a diabody, a monovalent single chain antibody, a diabody, a chain entibody or a chimerised antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as extracellular domain of the KDR receptor with the same affinity as extracellular domain of the KDR receptor with the same affinity as extracellular domain of VBGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 50; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor,
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29-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glioblastoma multiforme; hemangioblastoma; AIDS; central nervous system neoplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin; antibody; complementary determing region; CDR; VEGF; vascular endothelial growth factor; KDR; kinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2000
Anti-human VEGF receptor Flt-1 antibody CDR peptide sequence
                                 08-MAY-2000
                                                                                              AAY77582 standard;
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                                                               AAY77582
                                                                                                                                                                                                                                                                                                                                         immunoglobulins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to reduce tumour growth
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                                                                                                                                                                                                                                             Conservative
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                               (first entry)
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99US-0240736.
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a gene recombinant antibody that has specific reaction with human vascular endothelial growth factor (VEGF) receptor Flt-1. The antibodies are useful for disgnosis and as remedies for diseases due to abnormal neovascularisation such as proliferation or metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W0996005E=A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene recombinant antibodies, useful for diagnosis and as remedies for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-072431/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-NOV-1999.
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                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                             rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                      Antibody; human; vascular endothelial growth factor; VEGF receptor; Flt-1; neovascularisation; cell proliferation; metastasis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-human VEGF receptor Flt-1 antibody CDR peptide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retinopathy, premature retinopathy and psoriasis.
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                                                       (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                                                                                                                                                                                                                                                                                                                             retinopathy; psoriasis.
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Pred. No. 0.0063;
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     Nakamura
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RESULT 7
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Matches 10
The invention relates to a method for inhibiting the growth of non-solid tumous cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonis&s). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised
                                                                                                                                                                                   Inhibiting g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain hypervariable region; VL; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; complementarity determining region-1; CDR-1; mouse.
                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540770
                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US10504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200174296-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vascular endothelial growth factor receptor; cytostatic; light chain hypervariable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gs snw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a gene recombinant antibody that has specific reaction with human vascular endothelial growth factor (VEGF) receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene recombinant antibodies, useful for diagnosis and as remedies for diseases due to abnormal neovascularization e.g. proliferation or metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE13140 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metastasis of solid tumor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retinopathy, premature retinopathy and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eaction with human vascular endothelial growth factor (VEGE) recept lt-1. The antibodies are useful for diagnosis and as remedies for iseases due to abnormal neovascularisation such as proliferation or stastasis of solid tumor, arthritis in rheumatoid arthritis, diabetisting the promoter of the stastasis of solid tumor, arthritis in rheumatoid arthritis, diabetistic or premature continuations.
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CORNELL RES FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody murine light
                                                                                                                                                              growth of non-solid tumor cell useful to treat bone marrow h as leukemias or multiple myeloma comprises treatment with ist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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Pred. No.
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0.0063;
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Best Local S
Matches 10
                                                                                                                     Disclosure; Page 37;
                                                                                                                                          Treating or controlling an angiogenic dependent condition neoplasm, collagen-vascular or autoimmune disease) in mamm administering a combination of an antiangiogenic molecule chemotherapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                           colon carcinoma; ovarian carcinoma; neuroblglioblastoma multiforme; melanoma; therapy; complementarity determining region.
                                                                                                                                                                                                                                                                                             28-JAN-2000;
31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acut or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody murine light chain hypervariable region (VL) CDR-1 used in the
                                                                                                                                                                                                         WPI; 2001-514531/56
                                                                                                                                                                                                                                    Kerbel
                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vascular endothelial growth factor; angiogenesis; antiangiogentitumour; neoplasm; collagen-vascular disease; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGF antagonist antibody IMC-1C11 VL CDR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMC-1C11; chimeric antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of
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                                                                                                                                                                                                                                                                                             2000US-0178791.
2000US-0539692.
                                                                                                                                                                                                                                                                                                                                  2001WO-US02839.
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-mo варіепв.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse; human; antagonist; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
0.0063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence is humanised (VL) CDR-1 used - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiangiogenic;
                                                                                                                                                                     in mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease;
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The present sequence is that of complementarity determining region of the light chain variable region (see also AAB82702) of IMC-1011, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibod or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or

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controlling an angiogenic dependent condition by

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RESULT 9
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                                                                                            Sequence
                                                                                                                   The present invention relates to derivatives of an antibody against ganglioside GM2. The antibody may be a monoclonal antibody or its fragments. The antibody is combined with a radioactive isotope, protein or small drug in the treatment and diagnosis of cancer.
                                                                                                                                                                               Claim 4;
                                                                                                                                                                                                     Monoclonal antibodies against radioisotopes or proteins for
                                                                                                                                                                                                                                          WPI; 2001-266142/27.
                                                                                                                                                                                                                                                                    Hanai N,
                                                                                                                                                                                                                                                                                                                   30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                   05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                          WO200123431-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse ganglioside
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroblastoma, glioblastoma multiforme or melanoma (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, central nervous system tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regression or arrest of the condition while minimising operenting significant toxicity of the chemotherapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-angiogenic molecule and a chemotherapeutic agent,
                                                                                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK.
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                      SASSSVSYMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody light chain variable region CDR1.
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Pred. No.
                                                         Score 48;
Pred. No.
                                                                                                                                                                                                       ganglioside GM2 combined with drugs, treatment and diagnosis of cancer -
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                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lon carcinoma, prostate carcinoma, central nervous system tumour,
                                             DB 22;
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hes 0;
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0.0063;
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RESULT 11
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AAB78851
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                                                                                                                                                                                                                                                                                                   This invention relates to a reagent for detecting differentiation of CC monocytes and macrophages from haematopoletic stem cells, containing a substance which binds to human vascular endothelial growth factor (VEGF) receptor Flt-1. The invention also includes a method for diagnosing a CC disease in which the differentiation of monocytes and macrophages is implicated, using the method, containing a substance which binds to Flt-1 cC diagnosed using the method, containing a substance which binds to Flt-1 cC which may be diagnosed or treated include inflammation, delayed CC typersensitivity, malignant tumours and arteriosclerosis.

CC AAF70190 - AAF70244, AAF70251 and AAF70258 represent DNA sequences CC cligonuclectides used in the construction of the antibody. The monoclonal antibody is used in the reagent of the invention. PCR primers AAF70245 - CC AAF78870 (excluding AAF70251) are used in the isolation of the antibody. The monoclonal cCC cantibody is used in the reagent of the invention. PCR primers AAF70245 - CC AAF78870 (excluding AAF70251) are used in the isolation of the antibody.
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Substances binding to human vascular endothelial growth factor reflt-1, used for diagnosis and treatment of inflammatory diseases, arteriosclerosis, cancer and delayed hypersensitivity -
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shitara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  delayed hypersensitivity; malignant tumour; arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-human Flt-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB78851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB78851 standard; Peptide;
                                                                                  AAB78857
                                                                                                                                                                                                                                                                                                                                of the anti-human Flt-1 antibody.
                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 127; 164pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-080847/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (КУОМ ) КУОМА НАККО КОСУО КК
                                                                                                                                                                                                                                                                                                                                               sequences. Protein sequences AAB78848 - AAB78870 represent fragments
                                                                                                                                                                                                 μ
                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  riation; monocyte; macrophage; haematopoietic stem cell; cancer;
endothelial growth factor; VEGF; Flt-1; inflammation; antibody;
                                                                                  standard;
                                                                                                                                                                                                 SASSSVSYMH 10
                                                                                                                                                                  SASSSVSYMH 10
                                                                                                                                                                                                                                                                                                   10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibuya
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-JP03957.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0171709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody KM1732 L chain V region CDR 1 peptide
                                                                                  Peptide;
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Pred. No. 0.0063;
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                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                               Length 10;
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20-APR-2001 AAB78857;

(first entry)

Anti-human Flt-1

ant ibody

KM1750 L chain V region CDR

1 peptide

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Best Local S
Matches 10
                           Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR; foetak liver kinase; FLK-1 receptor; vascular endothelial growth factor; VEGF; tumour growth; light chain complementarity determining region 1; CDRL1; angiogenesis; plC11; scFv antibody.
                                                                                                                      Mouse
                                                                                                                                                      15-NOV-2002
                                                                                                                                                                                                                      AAE25952 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease in which the differentiation of monocytes and macrophages is implicated, using the reagent, and an agent for the treatment of diseases diagnosed using the method, containing a substance which binds to Flt-1 or a substance which inhibits the signal transduction of Flt-1. Diseases which may be diagnosed or treated include inflammation, delayed hypersensitivity, malignant tumours and arteriosclerosis.

AAF70190 - AAF70244, AAF70251 and AAF70258 represent DNA sequences encoding anti-human Flt-1 monoclonal antibody fragments, and oligonucleotides used in the construction of the antibody. The monoclonal antibody is used in the reagent of the invention. PCR primers AAF70245 - AAF78870 (excluding AAF70251) are used in the isolation of the antibody DNA sequences. Protein sequences AAB78848 - AAB78870 represent fragments of the anti-human Flt-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monocytes and macrophages from haematopoietic stem cells, containing a substance which binds to human vascular endothelial growth factor (VEC receptor F1-1. The invention also includes a method for diagnosing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Substances binding to human vascular endothelial growth factor receptor Flt-1, used for diagnosis and treatment of inflammatory diseases, arteriosclerosis, cancer and delayed hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer; vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody; delayed hypersensitivity; malignant tumour; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 128; 164pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-080847/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a reagent for detecting differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shitara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                      anti-KDR
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                                                                                                                                                                                                                                                                                                                                              SASSSVSYMH 10
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
A
                                                                                                                plC11 scFv antibody CDRL1 peptide
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                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Pred. No. 0.0063;
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RESULT 13
AAU74409
ID AAU74
AC AAU74
AC AAU74
XX Light
XX Compl
CKW Compl
KW angic
KW WEGF;
KW antik
XX WO20(
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity determining region; CDR; CDRL1; antigen; cytogtatic; angiogenesis inhibitor; vascular endothelial growth factor receptor; VEGF; tumour; leukaemia; antibody; cell proliferation inhibitogr;
                                                                                                                                      24-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR p1C11 scFy antibody
                                                                                                                                                                                            24-MAY-2001; 2001WO-US16924.
                                                                                                                                                                                                                                                   29-NOV-2001
                                                                                                                                                                                                                                                                                                         WO200190192-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU74409 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 11; 34pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel immunoglobulin molecule for reducing tumor growth, t kinase insert domain-containing receptor with an affinity human vascular endothelial growth factor, and neutralizes
                                                                                   (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD42817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-2000; 2000US-0493539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2002064528-Al.
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WITTE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   light chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AA;
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                                                                                                                                      2000US-206749P.
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                                                                                                                                                                                                                                                                                                                                                                                                                         variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determining region
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Pred. No. 0.0063;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L1 (CDRL1).
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2002-106189/14. DE, AAS20280.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complex of two polypeptides (P1) and two second polypeptides (P2) which CC are stably associated in an immunoglobulin like complex. P1 has an CC antigen-binding site located to the N terminus of immunoglobulin (Ig) CC light chain constant domain (CL domain), and P2 has an antigen-binding CC site located to the N terminus of the CH1 domain. (I) is useful for: CC neutralising the activation of a vascular endothelial growth factor CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; CC reducing endothelial cell proliferation; inhibiting VEGF induced CC migration of human leukaemia cells; blocking interaction of a protein and CC its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment CC methods. The design of (I) provides for efficient produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural CC antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. CC complementarity determining region L1 (CDRL1) incorporated into an contigen-binding protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                            Hiatt AC,
                                                                                                                                                            08-NOV-2001
                                                                                                                                                                                           WO200183806-A1
                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                        Immunoglobulin; antibody; light chain; heavy chain; CDR; FR; complementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
                                                                                                                                                                                                                                                                                                                                          Mouse Kappa VI
                                                                                                                                                                                                                                                                                                                                                                            14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                             AAU70361;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU70361 standard; Peptide; 10 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an antigen-binding protein (I) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           two
                                                                                                                            02-MAY-2001; 2001WO-US14349
                                                             (EPIC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bispecific immunoglobulin-like antigen-binding protein for reducing our growth and for inhibiting angiogenesis, comprises a complex of polypeptides and two second polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                             EPICYTE PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 56; 64pp; English.
                            Hein MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
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                                                                                            2000US-0563222
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                                                                                                                                                                                                                                                                                                                                          light chain
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                                                             INC.
                                                                                                                                                                                                                                                                                                                                            CDR1
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Pred. No. 0.0063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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Preparing immunoglobulin binding protein array in plant transforming the cells with different polynucleotides er protein polypeptides specific to ligand, selecting plant
                                                                                                                                                                        preparing array
                                                                                                                                                                            array in plant cells by lynucleotides encoding binding selecting plant cells for
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Disclosure; Page 14; 129pp; English

The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynuclectides encoding different immunoglobulin binding protein (IBBP) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transferted cells, to generate an IBBP that thinds to a ligand, and transferted plant cells are selected, and preparing an IBBP array in plant cells. At least one peptide sequence has at least 75% sequence identity to a framework region (FR) of a native IBW, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin protein array, preferably heavy chain binding protein (CHBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. Agrobacterium tumefaciens or maize) cor other eukaryotic cells (e.g. Agrobacterium seasys of IBBPs having desired characteristics. The present sequence is a mammalian IBBP of immunoglobulin derived peptide that may be incorporated into an IBBP of invention.

Sequence 10 ΑA;

Matches Query Match Best Local 10; Similarity Conservative 100.0%; Score 48; DB 23; 100.0%; Pred. No. 0.0063; 0 Mismatches DB 23; 0 Length 10; 0; Gaps

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밁 8 ш ч SASSSVSYMH 10 SASSSVSYMH

RESULT 15 ABJ26721

ABJ26721 standard; Peptide; 10 A

01-MAY-2003 (first entry)

VEGF binding related peptide SEQ ID No O

bispecific Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour; antigen-binding protein; murine

Mus

WO2003002144-A1

09-JAN-2003

26-JUN-2002; 2002WO-US20332

26-JUN-2001; 2001US-301299P.

(IMCL-) IMCLONE SYSTEMS INC.

Zhu

WPI; 2003-201468/19.

N-PSDB; ABT23299.

New bispecific antibodies having antigen-binding sites specific for first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -

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Claim 6; Page 48; 98pp; English.

XX
CC
The invention relates to a novel antibody having a first antigen binding
CC site specific for a first vascular endothelial growth factor (VEGF)
CC receptor and a second antigen-binding site specific for a second VEGF
CC receptor. The bispecific antigen-binding proteins block activation of the
CC vEGF receptor and are useful for reducing or inhibiting VEGF-induced
CC cellular functions such as mitogenesis of vascular endothelial cells
CC and migration of leukaemia cells. The antibodies are useful for treating
CC uncours and for in vivo or in vitro for investigative and diagnostic.
CC methods. This sequence represents a mouse peptide relating to the
CC bispecific antibodies that bind to the VEGF receptors of the invention.
XX
SQ Sequence 10 AA;

Query Match
Best Local Similarity 100.0%; Score 48; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 1 SASSSVSYMH 10
Search completed: July 30, 2003, 09:36:46
Job time: 11 secs
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g kappa chain
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g light chain
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l Similarity 100.0%; Pred. No. 0.0079; 10; Conservative 0; Mismatches 0; Indels 1 SASSSYSYMH 10 16 SASSSYSYMH 25	chain V region - mouse Mus musculus (house mouse) 2-Nov-1993 #sequence_revision 10-Nov-1 n: S17637 7.; Hoogenboom, H.R.; Griffiths, A. 2, 624-628, 1991 4aking antibody fragments using phage faking antibody fragments using phage ranmber: S17230; MUID:91326098; PMII preliminary preliminary type: nucleic acid s: 1-91 <cla> type: nucleic acid s: 1-91 <cla> thererotetramer; immunoglobulin main: immunoglobulin homology <imm></imm></cla></cla>	Query Match 100.0%; Score 48; DB 2; Length 91; Best Local Similarity 100.0%; Pred. No. 0.0079; . Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 SASSVSYMH 10	RESULT 1 S17629 Ig kappa chain V region - mouse C;Species: Mus musculus (house mouse) C;Accession: S17629 R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G. Nature#3527m6244628, x13924 A;Title: Making antibody fragments using phage display libraries. A;Reference number: S17230; MUID:91326098; PMID:1907718 A;Recession: S17629 A;Status: preliminary A;Residues: 1-91 <cla> C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology <imm></imm></cla>	ALIGNMENTS	30 48 100.0 107 2 S11113 Ig kappa chain V r 31 48 100.0 107 2 S11116 Ig kappa chain V r 32 48 100.0 107 2 S11117 Ig kappa chain V r 33 48 100.0 107 2 S11118 Ig kappa chain V r 34 48 100.0 107 2 S11119 Ig kappa chain V r 35 48 100.0 107 2 S11121 Ig kappa chain V r 36 48 100.0 107 2 S11123 Ig kappa chain V r 37 48 100.0 107 2 S11123 Ig kappa chain V r 38 48 100.0 107 2 PT0406 Ig kappa chain V r 39 48 100.0 107 2 G30560 Ig kappa chain V r 40 41 100.0 108 2 G30560 Ig kappa chain V r 41 47 97.9 107 2 PL0013 Ig kappa chain pre 42 47 97.9 107 2 PD0011 Ig kappa chain V r 43 45 93.8 91 2 S17628 Ig kappa chain V r 45 44 91.7 91 2 S17628 Ig kappa chain V r

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16 SASSSVSYMH 25

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Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Fe__1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
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C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: $20650
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, K-Ebruary 1997
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A;Accession: S20653
A;Status: preliminary
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R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from
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                                                                          A; Molecule type: DNA
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A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
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A; Residues: 1-91 < CLA>
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C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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;Cross-references: EMBL:X65009; NID:g52651; PIDN:CAA46142.1; PID:g52652
;Superfamኒኒኒ : immunoglobulin V region; immunoglobulin homology
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Pred. No. 0.0082
; Mismatches
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.0079;
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R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1084
                                                                                                         C;Keywords: immunog ניטיינים:
F;16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                  A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                Ig light chain V region (clone 202.61) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: PH1084
                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-97 <TIL>
                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown
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F;11-84/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-39,'K',41-97,'L' <CAT>
A;Residues: 1-39,'K',41-97,'L' <CAT>
A;Cross-references: EMBL:X59179; NID:g52311; PIDN:CAA41889.1; PID:g1334060
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A; Residues: 1-97 <STA>
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(Species: Mus musculus (house mouse)
(C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-jun-2000
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F;16-89/Domain: immunoglobulin homology <IMM>
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Local Similarity 100.0%; s
nes 10; Conservative 0;
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SASSSVSYMH 10
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ilarity 100.0%; Pred. No. 0.0085;
Conservative 0; Mismatcher
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                                                             100.0%; Score 48; DB 2; 100.0%; Pred. No. 0.0085;
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Pred. No. 0.0082;
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G;Date: 17-70...C;Date: 17-70...C;Date: 17-70...C;Date: 17-70...C;Date: 17-70...C;Date: 17-70...C;Date: 17-70...C.
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
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S11115
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submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S29590
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S29590
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A;Title: Common structural features among monoclonal antibodies binding A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: D38601
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C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
                                                                         A; Molecule type: mRNA
A; Residues: 1-102 < KAA>
                                                                                                                                                                                                                                                                                          Ig kappa chain V region (clone NQ2-20.5.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change
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A; Residues: 1-100 <KAV>
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                         Superfamily: immunoglobulin V region; immunoglobulin homology;16-84/Domain: immunoglobulin homology <IMM>
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S.C.; Retzel,
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Pred. No. 0.0088;
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Pred. No. 0.0087;
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                                                                                         Ig kappa chain V region (anti-idiotypic) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
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                                             C;Accession: B49049
R;Armandola, E.A.; Mariani, S.M.;
                                                                                                                                                                          B49049
                                                                                                                                                                                               RESULT 13
A;Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antige
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J. Immunol.

22, 2893-2899,

Zwickl, M.; Hardman, N.; Ferrone,

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A;Cross-references: EMBL:X58204
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-87/Domain: immunoglobulin homology <IMM>
                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-103 <KAN-1
A;Residues: 1-103 <KAN-1
A;Cross-references: EMBL:X59094; NID:g52227; PIDN:CAN-1820.1; PID:g52228
A;Cross-references: EMBL:X59094; NID:g52227; PIDN:CAN-1820.1; PID:g52228
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                            Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
C;Accession: S29591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995
                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                           A; Reference number: A; Accession: S29591
                                                                                                                                                                                                                                                                           submitted to the EMBL Data A; Reference number: S26459
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A;Title: Deletions of immunoglobulin C(kappa) region characterized
A;Reference number: S24214; MUID:91217618; PMID:1902500
A;Accession: S24214
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R;Shimizu, T.; Iwasa
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                                                                                  Query Match
Best Local Similarity
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Pred. No. 0.0091;
Mismatches 0
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Pred. No.
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Pred. No.
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-89/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Datc: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
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R;Levy, S.; Campbell, M.J.; Levy, R.

J. Exp. Med. 170, 1-13, 1989

A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangements, PS0071

A;Reference number: A92781; MUID:89310348; PMID:2501443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescA;Reference number: A54378; MUID:94165109; PMID:7509814
A;Accession: B54378
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A;Note: sequence extracted from NCBI backbone (NCBIN:118298, NCBIP:118299)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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A;Accession: B49049
A;Status: preliminary
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A;Residues: 1-106 <AGA>
A;Residues: 1-106 <AGA>
A;Cross-references: GB:S68985; NID:g545746; PIDN:AAB30096.1; PID:g545747
A;Coss-references: spleen and myeloma cell line MOPC 315.43
A;Experimental source: spleen and myeloma cell line MOPC 315.43
A;Note: sequence inconsistent with nucleoride translation
A;Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 06-00t-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
                                                                                                                                                                                          A; Residues: 1-106 <LEV>
                                                                                                                                                                                                                   A; Molecule type: DNA
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  100.0%; Score 48; DB 2; Length 106; ilarity 100.0%; Pred. No. 0.0094; Conservative 0; Mismatches 0; Indels
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Search completed: July 30, 2003, 09:44:07 Job time : 2.95681 secs

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Result
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Listing first 45 summaries
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RESULT 2

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                 MEDLINE=81054757; PubMed=6776525;
Rudikoff S., Rao D.N., Glaudemans C.P.J.
"Kappa Chain joining segments and struc
combining sites.";
Proc. Natl. Acad. Sci. U.S. A. 77:4270-4
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Rao D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three
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Rao D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three
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COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-1.
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Sciurognathi;
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=83271467; PubMed=6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response
phenyloxazolone and its early diversification.";
  NCBI_TaxID=10090;
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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MEDLINE=83271467; PubMed=6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
                                                                                                  Kaartinen M., Griffiths G.M., Markham A.F., Milstein "mRNA sequences define an unusually restricted IgG rephenyloxazolone and its early diversification.";
           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
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Ig_MHC.
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Pred. No.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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Pred. No. 0.0029
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RESULT 11

KV6E_MOUSE!

ID FV6B

AC P016:
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DT 21-J

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KV6K_MOUSE
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Best Local
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                                                                           21-JUL-1986 (Rel. 01, Created)
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28-FEB-2003 (Rel. 41, Last ann
19 kappa chain V-VI region J53
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MEDLINE=83271467; PubMed=6877353;
MEDLINE=83271467; PubMed=6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein
"mRNA sequences define an unusually restricted IgG re
phenyloxazolone and its early diversification.";
                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin
DOMAIN 1
DOMAIN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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P04945;
    MEDLINE=81054757; PubMed=6776525;
                SEQUENCE.
                                   NCBI_TaxID=10090;
                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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SMART; SM00406; IGv;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia;
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STANDARD;

PRT;

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Gluconate transport i GTI1 OR SPAC1751.01C. Schizosaccharomyces p

Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

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SMART; SM00406; IGv;
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PDB; 2FBJ; 15-OCT-90.
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MEDLINE=88217852; PubMed=3449853;
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                                                             1 SASSSVSYMH
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8; Conser
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IPR003006;
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COMPLEMENTARITY-DETERMINING-3
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-1.
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structural diversity of antibody
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Schizosaccharomycetaceae;

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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Rabrooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Mones L., Jones M., Leather S., Nightt D., Odell C., RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA Mooney P., Simonds M., Squares R., Squares S., Stevens K., RA Ra Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Skelton J., Simonds M., Squares R., Squares S., Stevens K., RA Weltjens I., Vanstreels B., Rieger M., Schaefer M., Mueller-Auer S., RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Giffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Detashkin J., RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., "The genome sequence of Schizosaccharomyces pombe."; RT Nature 415:871-880 (2002)
                                                                                                                                   Matches
                                                                                  Best Local
                                                                                                 Query Match
                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                  SEQUENCE
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EMBL; AL133154; CAB61447.1;
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SIMILARITY: IN THE N-TERMINAL REGION; TO S.POMBE PAC2.
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RESULT 13 KV4A_MOUSE

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P01680;
21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
            N-acetylmuramoyl-L-alanine
Bacteriophage rlt.
Viruses; dsDNA viruses, no
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DOMAIN
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SMART; SM00406; IGv;
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HSSP; P01679; 2FBJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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"Two kappa immunoglobulin
Cell 26:57-66(1981).
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PS50835; IG_LIKE;
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E., Seidman J.G
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annotation updat
S107B precursor.
                                                     annotation update) amidase (EC 3.5.1.28).
                RNA stage; Caudovirales; Siphoviridae
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FRAMENK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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RESULT 15
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                      modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malus domestica (Apple) (Malus sylvestris). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Aggroliophyta; eudicotyledons; core eueurosids I; Rosales; Rosaceae; Maloideae; Malus.
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Pfam; PF01510; Amidase_2;
Pfam; PF01544; Ami_2; 1.
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SEQUENCE FROM N.A.
MEDLINE=96332669; PubMed=8730875;
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                      Plant Physiol. 106:521-528(1994).
-!- FUNCTION: Involved in cell wall degradation. Degrades polysaccharides containing beta-(1-->4)-linked galacta
                                                                                                                                                                                                                                                                                                      STRAIN=cv. Granny Smith; TISSUE=Fruit cortical tissue; MEDLINE=95083752; PubMed=7991682; MEDLINE=95083752; PubMed=7991682; Ross G.S., Wegrzyn T., Macrae B.A., Redgwell R.J.; "Apple beta-galactosidase. Activity against cell wall polysaccharides and characterization of a related cDNA clone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00644; Ami
Hydrolase; Cell wall
SEQUENCE 270 AA;
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Mol. Microbiol. 19:1343-1355(1996).
-I- CATALYTIC ACTIVITY: Hydrolyzes the
residues and L-amino acid residues
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                    European Bioinformatics Institute. There are no restrictions on by non-profit institutions as long as its content is in no ified and this statement is not removed. Usage by and for commen
                                                                                                                                                 galactose residues in beta-D-galactosides.
SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                        as an exo-(1-->4)-beta-D-galactanase.
CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing galactose residues in beta-D-galactosides.
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SIMILARITY: BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE
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tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce,
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Pred. No. 7.4;
2; Mismatches
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in certain bacterial cell-wall
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                                                                                                                    SIGNAL
                                                                                                                              Hydrolase; Glycosidase; Signal.
                                                                                                                                      PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.
                                                                                                                                                                              PIR; T17002;
                                                                                                                                                                                        EMBL; L29451; AAA62324.1;
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                                      h 70.8%;
Similarity 70.0%;
7; Conservative
                 SASSSVSYMH
AASASVSYDH
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251
731 AA;
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PROTON DONOR (POTENTIAL).
NUCLEOPHILE (POTENTIAL).
                                                Score 34;
Pred. No.
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                                       Mismatches
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   of hits satisfying chosen parameters:
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6: sp_mammal:*
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EMBL; AF516285; AAM642.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
TPR003006; Ig_MHC.
TPR003006; Ig_MHC.
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Pred. No. 0.021;
Mismatches 0;
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InterPro; IPRO03599; Ig. InterPro; IPRO07110; Ig-like. InterPro; IPRO07110; Ig_MHC. InterPro; IPRO03596; Ig_V. InterPro; IPRO03596; Ig_V. Pfam; PF00047; Ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Q8VDD0;
01-MAR-2002
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Zhou Y.-X., Taguchi H., Planque S., Kar
"Innate proteolytic antibodies: Failed
entantiomer of VIP and identification o
Submitted (MAY-2002) to the EMBL/GenBan
EMBL, AF516283; AAM64201.1; -.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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Mus musculus (Mouse).
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
Anti-MCG ZI2 variable light
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Mammalia; Eutheria;
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Rodentia;
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Rodentia;
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23, Last annotation update)
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Karle S., Nishiyama
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                                                                                                                                                                     Q91W12 PRELIMINARY; PRT; 235 AA.
Q91W12;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Unknown (Protein for MGC:6582).
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SEQUENCE
                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                   SEQUENCE FROM N.A.
TISSUE=Breast tumor;
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SMART; SM00406; IGV;
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EMBL; AF206030; AAF69328.1; -.
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Mammalia; Eutheria;
                  Strausberg R.,
                                                                                        NCBI_TaxID=10090;
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01-OCT-2000
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InterPro; IPR003006;
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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                                                                                                                   Chordata;
Rodentia;
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Rodentia;
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100.0%;
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Ig_MHC.
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90.0%;
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Pred. No. 0.12;
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Pred. No.
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Sciurognathi; Muridae;
                                                                                                                 Sciurognathi;
                                                                                                                                    Craniata;
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thi; Muridae; Murinae;
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; Murinae; Mus.
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(APR-2001) to the EMBL/GenBank/DDBJ databases.

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Best Local S
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Best Local S
Matches
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                 Q9U410
Q9U410;
01-MAY-2000
         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 immunoglobulin
variable region (Fragment).
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenes
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                         PROSITE;
NON_TER
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC006643; AAH06643.1; -
InterpSo; IPR007110; Ig-like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-2002) to the EMBL; AF516282; AAM64200.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S
"Innate proteolytic antibodies: Failed D-VIPase response to the D-
entantiomer of VIP and identification of L-VIPase VL domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TYEMBLrel. 22, Created)
01-OCT-2002 (TYEMBLrel. 22, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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9; Conserv
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112 /
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90.0%;
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Pred. No. 0.52
1; Mismatches
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Pred. No.
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                      Trematoda; Digenea;
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Q9V4Z9 PRELI
Q9V4Z9;
01-MAY-2000 (TrEN
01-MAY-2000 (TrEN
01-OCT-2002 (TrEN
CG11770 protein
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Q59117;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
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                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actino Micrococcineae; Micrococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Song X.T., Feng Z.Q., Qi
"Amplification, cloning
variable region gene of
                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                InterPro; IPR000172; GMC_oxred.
Pfam; PF00732; GMC_oxred; 1.
PROSITE; PS00624; GMC_OXRED_2; 1.
Oxidoreductase.
                                                                                                                                                                                                                                         EMBL; X84895; CAA59321.1; -. HSSP; P22637; 3COX.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1665;
                                                                                                                                                                                                                                                                                                                                                                   Arthrobacter globiformis.
                                                                                                                                                                                                                                                                                                                                                                               CODA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                      MEDLINE=96145502; PubMed=8555454;
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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InterPro; IPR003596; Ig_v.
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InterPro; IPR007110; Ig-like.
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T; SM00406; IGv; 1.
                                                                                                      208 SSSSVSYIH
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6 (TrEMBLrel. 01, Las
1 (TrEMBLrel. 19, Las
idase (EC 1.1.3.17).
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106 AA;
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 (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
tein (LINES).
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11478 MW; F20F544426BAE63E CRC64;
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77.8%;
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80.0%;
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           Created)
Last sequence update)
Last annotation updat
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                                                                                                                                             Score 37; DB Pred. No. 23; 2; Mismatches
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Pred. No.
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ed. No. 2.5;
Mismatches
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                                                                                                                                                                                                                                                                                            Mustardy L.,
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                                                                                                                                                                  Length 547;
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RA Addms N.D., Celniker S.E., Holt R.A., Sabburner M., Henderson S.N.,
RA Admanatides P.G., Scherer S.E., Holt R.A., Sabburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Ffeifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Ffeifer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Herriardez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibeyama C.,
RA Kinmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Siden-Kiamos I., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Weinsehn D.A.,
RA Mang S.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Pandon M., Zhu S., Zhu S., Zhu O., Zheng L.,
RE Schen S., Spradling A.G., Stapleton M., Smith H.
                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Q9VIF5;
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Hatini V., Bokor P., Goto-Mandeville R., DiNardo S.;
"Tissue- and stage-specific modulation of Wingless signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome sequence of Dros
Science 287:2185-2195(2000).
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                  366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nt polarity gene lines.";
Dev. 14:1364-1376(2000).
AE003835; AAF59024.1; -.
AF272358; AAF76228.1; -.
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¬ PRELIMINARY;
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Pred. No.
                                     PRT;
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                                     981 AA
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RA Abril J.F., Abayani A. An H.-J. Andrews-Pfannkoch C.R., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov Si, RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov Si, RA Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Delcher A., Deng Z., Mays A.D., Dew I. Dietz S.M., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dunkov B.C., Dunn P., RA Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glasn P., Harris M., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchim K.A., RA Harris N.L., Harvey D., Heimann T.J., Hernandez J.R., Houck J., Li Z., Liang Y., Lin X., Li X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Shen H., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sin E., Shen H., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Yelbay K.H., Zhong F.N., Zhong W., Zhang G., Zhao Q., Zhéng L., RA Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C., Ra Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C., Shence 287:2185-2195 (2000).
                                                                                             Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Revans C.A., Gocsyne J.D., Amanatides P.G., Brandon R.C., Rogegs Y.,

Ramson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,

Revariera S., Frise B., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Woy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Woy M., Murphy B., Nelson C., Tyler D.,

A Phouamenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Champe M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

"Sequencing of Drosophila melanogaster genome.",

"Sequencing of Drosophila melanogaster genome.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
                  [3]
SEQUENCE FROM N.A.
Crosby M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Brachycera; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Misra S., Crosby M.
Hradecky P., Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Υ.Α
Matthews B.B.,
Kaminker J.S.,
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Prochnik S.E., Sm
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  L., Campbell K.,
Smith C.D.,
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QUBOO3
ID QOBOO
AC QOBOO
AC QOBOO
DT O1-NC
DT O1-JU
DE Chrom
GN YLRO7
OS Sacch
OC Eukar
OC Sacch
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(1) RN
(1) RN
(2) SEQUE
RA MIPS;
SQ SEQUE
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Best Local (
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Q08003;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-UUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                      Q8T6L8 PRELIMINARY; PRT; 689 AA.
Q8T6L8;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Unconventional myosin 29D short isoform.
D OR M7029D OR CG10595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2002) to the EMBL/GenBank/DDBJ EMBL; AE003669; AAF53964.2; - FlyBase; FBgn0032920; CG9252. SEQUENCE 981 AA; 110816 MW; 9A825881240BDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1996) to the EMBL/GenBank/DDBJ
EMBL; Z73245; CAA97630.1; -.
SGD; S0004063; YIR073C.
SEQUENCE 200 AA; 22850 MW; 1C93378ED78C41A
                                                                              Eukaryota; Metazoa;
                                                                                                       Drosophila melanogaster (Fruit fly).
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Saccharomycetales;
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D., Celniker S.E., G
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                                                                              Arthropoda;
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EMBL/GenBank/DDBJ
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Pred. No. 71;
1; Mismatches
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Pred. No.
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cetaceae; Saccharomyces.
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                                                                              Hexapoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                              Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Thus
J QBT6L9
C QBT6L9;
JT 01-JUN-2002 (TrEMBLrel. 21, Createw,
JT 01-JUN-2002 (TrEMBLrel. 21, Last sequence upward)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation upo
DE Unconventional myosin 29D.
GN D OR MY029D OR CG10595.
OS Drosophila melanogaster (Fruit fly).
Privaryota; Metazoa; Arthropoda; Hexapoda; Ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
084646
                                                                              CAPPERE
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                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O84646;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
Exodeoxyribonuclease V, gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IFR001609; myosin_head.
Pfam; PF00063; myosin_head; 1.
ProDom; PD000355; myosin_head; 1.
SMART; SM00242; MYSC; 1.
SEQUENCE 689 AA; 74009 MW; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Romitchell W.P., Olinger L., Tatusov R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myosins.";

Mol. Biol. Evol. 0:0-0(2002).

EMBL; AF454349; AAL91723.1; -.

FlyBase; FBgn0000410; d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 282:754-759(1998).
EMBL; AE001334; AAC68244.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Chlamydiae;
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Oregon R; TISSUE=Ovary;
Tzolovsky G., Bownes M., Millo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      084646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of an obligate Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
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1004 AA; 114401 MW;
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phylogenetic ar
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70.0%;
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                                                                                                                                                                      Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; D
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9525A3C5B928FD2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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.., Zhao (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2e+02;
                                                                           Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                      update)
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Drosophila
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Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 689;
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RESULT 15
Q813Q2
Q813Q2
Q813Q2
Q813Q2
Q813Q2
Q813Q2
Q813Q2
Q913Q2
                                                                                                                                                                                        WREDLINE=2225708; PubMed=12368867;

WA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,

WA Mangall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,

WA London Burrows C., Cherevach I., Chillingworth C.,

WA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,

WA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,

WA Cronin A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

WA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,

WA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,

WA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,

WA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,

WA Harper D., Hauser H., Wonnes K.D., Johnson D., Kerhornou A.,

WA Harper S., Jagels K., James K.D., Johnson D., Kerhornou A.,

WA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

WA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,

WA Line A., Maddison M., Mclean J., Rabbinowitsch E.,

WA Cliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,

WA Cliver K., Sharp S., Smith R., Squares R., Sguares S., Stevens K.,

WA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,

Washing A., Newbold C., Barrell B.G;

"Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
          Query Match
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pfam; pr00613; myosin_head; 1.
proDom; p000035; myosin_head; 1.
swhart; sw00015; IQ; 1.
swhart; sw000242; MYSC; 1.
pr0SITE; pS50096; IQ; 1.
sEQUENCE 1313 AA; 142708 MW; 12
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Devlin K., Baker S., I

Hall N., Bowman S., Cl

Submitted (SEP-2002) t
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Q813Q2;
                                                                       Hypothetical SEQUENCE 53
                                                                                                                                       Nature 419:527-531(2002).
EMBL; AL929353; CAD51575.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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01-MAR-2003
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Mol. Biol. Evol. 0:0-0(2002).
EMBL; AF454348; AAL91722.1; -.
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STRAIN=Oregon R; TISSUE=Ovary;
Tzolovsky G., Bownes M., Millo H., Pathira
"Identification and phylogenetic analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR000048; IQ_region.
interPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lyBase; FBgn0000410; d.
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                                                                       al protein.
518 AA; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                       63009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.9%;
       70.8%;
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23,
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Last annotation update)
   Score 34;
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Pred. No. 1.6e+02;
4; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                       8AE81B1DD59638D7 CRC64;
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nalysis of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518 AA
DB 5; Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berriman M., Pain Barrell B.;
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                                   Best Local Similarity
Matches 7; Conserv
113 ŚŚŚŚŚYŚYKH 122
                 SASSSVSYMH
                                    Conservative
                 10
                                             70.0%;
                                   Pred. No. 95;
1; Mismatches
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                                    Indels
                                    0; ; Gaps
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Search completed: July 30, 2003, 09:42:38 Job time: 10.852 secs



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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34; Search time 3.22259 Seconds (without alignments)
131.295 Million cell updates/sec

Sequence: Title: Perfect score: US-09-865-198-4 SASSSVSYMH 10

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

328717 seqs, 42310858 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/FCTUS_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

27		25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	σ	ۍ.	4.	w	N	1	No.
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1 SASSSVSYMH 10

Gaps

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US-07-634-278-1 US-07-634-278-7 US-07-634-278-16 US-07-634-278-16 US-08-477-728-1 US-08-477-728-7 US-08-477-728-16 US-08-477-728-16 US-08-477-728-16 US-08-477-040-1 US-08-474-040-1 US-08-474-040-1 US-08-474-040-1 US-08-474-040-1 US-08-474-040-1 US-08-474-040-1 US-08-487-200-7 US-08-487-200-1 US-08-487-200-16 US-08-488-113B-163

ALIGNMENTS

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RESULT 1
US-08-116-778E-9
                                                                                    US-08-116-778E-9
                                                                                                                                     REFERENCE/DOCKET NUMBER: 249-
TELECOMMUNICATION INFORMATION:
TELESHONE: (703)816-4000
TELESHAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOY: 11 toes
                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION UNMBER: 32,955
REGISTRATION UNMBER: 32,955
Query Match 100.0%; S
Best Local Similarity 100.0%; F
Matches 10; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08116778E Patent No. 5830470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: NAKAMUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASBGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA
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KUWANA, YOSHIHISA
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  Score 48; DB 2; 1
Pred. No. 0.0046;
); Mismatches 0;
                                      Length 10;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide -08-438-562-9
                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION UNDER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
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UMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US, FILING DATE: 10-MAY-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
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                                                                                                                                 No.
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                                                                                                                                    7, Application US/08483528B 5939532
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1100 NORTH GLEBE ROAD
                                                                     NAKAMURA, KAZUYASU
KOIKE, MASAMICHI
SHITARA, KENYA
                                                                                                                                                                                                                                                                                                                                                                                                         10 amino acids
          KUWANA, YOSHIHISA
HASEGAWA, MAMORU
VENTION: HUMANIZED ANTIBODIES
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                                                         , NOBUO
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Best Local Similarity 100.0%;
Matches 10; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703)816-410 INFORMATION FOR SEQ ID NO:
                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stan
REGISTRATION NUMBER: 25,
                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Antibody Against Human Interleukin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                  APPLICATION NUMBER: JP 2 FILING DATE: 11-SEP-1995
                                                                                                                     APPLICATION NUMBER: US/08/836,561 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                          COUNTRY: U
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TELEFAX: (703)816-4100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: VIRGINIA COUNTRY: U.S.A.
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1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                          USA
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HANAI, No. 6018032uo
TAKATSU, Kiyoshi
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IIDA, Akihiro
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55 Avenue of the Americas
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Pred. No. 0.0046;
); Mismatches 0
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                                                           Query Match
Best Local S
Matches 10
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Best Local Similarity
                                                                                                                       -09-393-385B-108
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                                                                                                                                                                                            TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 10 aming acids
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                          STATE: V. S.A. COUNTRY: U.S.A. 22201-4714
                                                                                                                                                                                                                                                         TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                    TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                               LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 NOI
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 70 SLECCMMUNICATION INFORMATION: 212-790-9090
                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-869-9741
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5. 6423511
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                            1 SASSSVSYMH 10
                                                                         Similarity
SASSSVSYMH 10
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1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                          1: (703)816-4000
(703)816-4100
                                                                                                                                               sos: single
linear
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                                                           Conservative
                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                       27-JUN-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YOSHIHISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 48; DB 3; Length 10; 100.0%; Pred. No. 0.0046;
                                                                      100.0%; Score 48; DB 4;
100.0%; Pred. No. 0.0046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KENYA
                                                                                                                                                                                                                                                                                                                       US/09/393,385B
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                                                                                      Length 10;
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                                                         Gaps
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SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-434-122-49
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US-09-280-028-4
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               Sequence 4, Application US/09280028
PATENT NO. 6241961
GENERAL INFORMATION:
APPLICANT: BENES, IVAN FRIEDRICH
APPLICANT: BOSSLET, KLAUS
TITLE OF INVENTION: METHOD FOR THEIR PREPARATION
FILE REFERENCE: BENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 49, Application Patent No. 6538111
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
CURRENT APPLICATION NUMBER: US/09/280,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM COMPACIBLE
COMPUTER: IBM COMPACIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/434,122
FILING DATE: 05-No. 653811-1999
PRIOR APPLICATION UMBER: 08/836,561
APPLICATION NUMBER: 08/836,561
FILING DATE: 09-MAY-1997
APPLICATION UMBER: JP 232384/95
FILING DATE: 11-SEP-195
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%;
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KOIKE, Masamichi
                                                                                                                                                                                                                                                                                        1 SASSSVSYMH 10
                                                                                                                                                                                                                                                                   SASSSVSYMH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 212-790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09434122
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IIDA, Akihiro
ANAZAWA, Hideharu
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                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 48; DB 4; 100.0%; Pred. No. 0.0046;
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EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
LENGTH: 97
Query Match
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Best Local &
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                                                                                                                                                                                            APPLICATION NUMBER: DE P4118120.4
FILING DATE: 03-JUN-1991
ATTORNEY_AGENT INFORMATION:
NAME: Kulik, David J.
REGISTRATION NUMBER: 36,576
REFERENCE_JOCKET NUMBER: 05552-1186
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 199 11
EARLIER FILING DATE: 1999-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus musculus
                                               TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/891,739
FILING DATE: 01-JUN-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR TOTATION NUMBER: DE CA110020
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tetravalent
TITLE OF INVENTION: Preparation
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                TELEPHONE: 202-1.
TELEPHONE: 202-408-4400
TO NO:
                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005-3315
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                                                                                                                 ENGTH:
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5959083
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                                                                                               amino acid
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                                                                  linear
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                                                                                                            amino acids
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                                                                              single
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100.0%;
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Pred. No.
Score 48;
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Length 100;
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RESULT 10
US-09-312-157-12
; Sequence 12, Application US/09312157
; Patent No. 6303341
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              TELEX: SEQUENCE LISTING INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: i
PRIOR APPLICATION DATA: i
PRIOR APPLICATION DATA: d
APPLICATION NUMBER: 08/
FILING DATE: 12/30/94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (619) 552-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
SOFTWARE: WORD PO
                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 633 West Fifth
STREET: Suite 4700
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                                                                                                            24 SASSSVSYMH
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                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                    DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
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                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                single
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, THOMAS LEHNER
IMMUNOGLOBULINS CONTAINING PROTECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM P.C. DOS 5.0
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: described below:
08/367,395
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                                                                                                                                                                                                                                                    Guy's 13 Kappa
                                                                                                                                                                                       Score 48; DB 3;
Pred. No. 0.053;
                                                                                                                                                                          Mismatches
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US-09-312-157-12
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                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE LISTING INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                          APPLICANT: NAKAMURA, Kazuyasu
APPLICANT: IIDA, Akihiro
APPLICANT: ANAZAWA, Hideharu
APPLICANT: HANAI, No. 6018032uo
APPLICANT: TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
TITLE OF INVENTION: Receptor Alpha Chain
                                                   CORRESPONDENCE ADDRESS:
                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/434,000
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: Guy's 13 Kappa SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPÉICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR ÜSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                     24
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
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New York
                                                                                                                                                                                                                                                                                                                                                                                     SASSSVSYMH 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word Perfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 67-351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 552-0159
                                                                                                                                                                                                                                                                                          Application US/08836561
                 B: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                 FURUYA, Akiko
                                                                                                                                                                                                                                  KOIKE, Masamichi
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Pred. No. 0.053;
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US-09-434-122-33
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Sequence 33, Applicati
Patent No. 6538111
GENERAL INFORMATION:
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APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
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REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 100.0%; Score 48; DB 3; Length 110; Local Similarity 100.0%; Pred. No. 0.056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 212-869-9741
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                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: PSALSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/434,122
FILING DATE: 05-No. 6538111-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ZIP: 10036
                                                                                                                                                                                                                                     CITY: New York
STATE: NY
APPLICATION NUMBER: 08/836,561
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HANAI, No. 6538111uo
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                                                                                   INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                              SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acid
TYPE: amino acid
                                                                                                                                 NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 24:0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
COLECULE TÝPE:
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                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: ARLINGTON
                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 33:
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TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
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                                                                                                                                                                                                                                                                                                                                                                                           VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
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                                               129 amino acids
                                                                               (703)816-4100
(703) 816-4100
77 TD NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                            1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KUWANA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOIKE, MASAMICHI
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                 linear
                                                                                                                                                                                                                                        07-SEP-93
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                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: NAKAMU
                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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CITY: ARLINGTON
STATE: VIRGINIA
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LOCATION:
                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 22201-4714
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                           HASEGAWA, MAMORU
VENTION: HUMANIZED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHITARA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOIKE, MASAMICHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAKAMURA, KAZUYASU
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                                                                                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "HYPERVARIABLE REGION 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "HYPERVARIABLE REGION 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED CONSENSUS
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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RESULT 15
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OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-438-562-2
                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-483-528B-92
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 92,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 48; DB 2; Length 129; Best Local Similarity 100.0%; Pred. No. 0.066; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: NAKAMU
APPLICANT: KOIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                     APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              APPLICANT:
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LOCATION: 24..33
IDENTIFICATION METHOD:
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PELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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LOCATION: -22..-1
                                                                                                                                                STREET: 1100 NOI
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                         COUNTRY:
                                                                                                                                                                                    ADDRESSEE:
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                                                                                                           VIRGINIA
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                                                                                                                                                             E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                            SHITARA, KENYA
HANAI, NOBUO
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KOIKE, MASAMICHI
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                                                                                                                                                                                                                                                                           KUWANA, YOSHIHISA
PatentIn Release #1.0, Version #1.25
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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Search completed: July 30, 2003, 09:38:29 Job time : 4.22259 secs

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US-08-483-528B-92
                                                                    Matches
                                                                                                  Query Match
                                                                                    Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
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LOCATION: 24..33
IDENTIFICATION METHOD:
LDENTIFICATION METHOD:
IDENTIFICATION METHOD:
OTHER INFORMATION: /pro
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APPLICATION NUMBER: US
FILING DATE: 07-JUN-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
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NAME/KEY:
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LOCATION: 88.96
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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LOCATION: 49..55
IDENTIFICATION METHOD:
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46
                                                                  10;
                                1 SASSSVSYMH 10
                                                                                    Similarity
SASSSVSYMH
                                                                    Conservative
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                                                                                  100.0%; Score 48; DB 2; 100.0%; Pred. No. 0.066;
                                                                                                                                                      /product= "HYPERVARIABLE REGION
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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                                                                    Ö
                                                                  Mismatches
                                                                    0
                                                                                                    Length 129;
                                                                  Indels
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                                                                  Gaps
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OM protein -

protein search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Minimum
Maximum
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No.
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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 1 US-09-798-689-4
5 US-10-195-752-108
US-10-160-232-12
5 US-10-160-232-13
5 US-10-283-349-49
US-09-986-107-12
9 US-09-976-787-24
10 US-09-9865-198-23
11 US-09-798-689-8
10 US-09-144-886-82
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US-09-563-222-41
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Sequence 4, Appli
Sequence 4, Appli
Sequence 41, Appli
Sequence 108, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 14, Appli
Sequence 24, Appli
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Sequence 23, Appli
Sequence 23, Appli
Sequence 8, Appli
Sequence 82, Appli
Sequence 82, Appli
Sequence 83, Appli
Sequence 83, Appli
Sequence 83, Appli
                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEG ID NOS: 40
SOTTWARE: WordPerfect 8.0 for Windows
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                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mus musculus US-09-976-787-4
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                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
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Best Local S
Matches 10
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	-09-910-059-	-232-	9-910-	-09-910-059-	US-09-910-059-61	-910-059-	187-	US-09-910-059-26	US-10-162-889-6	US-09-808-037-6	US-10-162-889-28	US-09-808-037-28	US-10-259-087A-20	US-09-865-198-27	US-09-976-787-28	US-09-798-689-21	US-09-865-198-28	US-09-976-787-29	US-10-195-752-113	US-10-195-752-111	US-10-160-232-92			-10-160-23	0-160-232-	US-10-160-232-89	-10-283-349-	US-09-865-198-8	09-976-787-8	US-09-144-886-88
4	9	equence 4,	e 71,	65	Sequence 61, Appl	50,	Sequence 8, Appli	Sequence 26, Appl	ტ ი	σ	Sequence 28, Appl	28	Ŋ	o N	õ	N	e 2	ĕ	_	1	Sequence 92, Appl	œ,	equence 90	φ	9	Sequence 89, Appl	μ	e œ	8	Sequence 88, Appl

ALIGNMENTS

Application US/09976787

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US-09-865-198-4
                Sequence 4, Application US/09865198 Patent No. US20020103345A1 GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
                                                                                                                                                                                          l Similarity
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; ORGANISM: Mouse
US-09-865-198-4
                                                                                                    TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/401,163
PRIOR APPLICATION NUMBER: 09/401,163
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATE: 1999-09-22
                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09798689
Publication No. US20030103973A1
GENERAL INFORMATION:
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Best Local Similarity
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Publication No
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Best Local Similarity
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SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 310098.406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.
                                                                           PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hiatt, Andrew
APPLICANT: Hein, Mich B.
TITLE OF INVENTION: IMMUNOGLOBULIN B:
TITLE OF INVENTION: EUKARYOTIC CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
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PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mus musculus
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                                      APPLICATION NUMBER: 08/
FILING DATE: 1996-09-03
FILING DATE:
                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SASSSVSYMH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FastSEQ for Windows Version 4.0
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No: US20030079253A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 48; DB 10; ilarity 100.0%; Pred. No. 0.0069; Conservative 0; Mismarchoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 48; DB 11; 100.0%; Pred. No. 0.0069;
                                                                                                  08/967,113
                   08/476,533
                                                            08/706,804
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SASSSVSYMH 10

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TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-195-752-108
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Query Match
Best Local Similarity
Matches 10; Conserv
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SEQ ID NO 4
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Best Local Similarity
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                                                                                                                                                                                                    APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEPAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/195,752
FILING DATE: 16-Unl-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAMURA, KAZUYASU
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                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: ARLINGTON STATE: VIRGINIA
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                                                                                                                                                                                 LENGTH: 10 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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100.0%; Score 48; DB 15; ilarity 100.0%; Pred. No. 0.0069; Conservative 0; Mismatches 0
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HANAI, NOBUO
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Pred. No. 0.0069;
                                     DB 15;
                                     Length 10;
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US-10-160-232-12; Sequence 12, Applicat; Publication No. US200; GENERAL INFORMATION:
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                                                          SEQ ID NO 18
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APPLICANT: ITO, MIKITO
APPLICANT: HANAI, NOBUO
                                                                                                     PRIOR APPLICATION NUMBER: 09/315,051
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/119,014
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: PCT/JP97/04259
PRIOR FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/160,232
CURRENT FILING DATE: 2002-66-04
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR FILING DATE: 1999-12-03
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CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR FILING DATE: 1999-12-03
                                                                                                                                                                                                                                                                                                                                              APPLICANT: HANAI, NOBUO
APPLICANT: KAWADA, YOKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHIBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
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APPLICANT: SHIBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHITARA, KENYA
APPLICANT: ITO, MIKITO
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                                                                                   SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Artificial Sequence
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                                        ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/315,051
FILING DATE: 1999-05-20
APPLICATION NUMBER: 09/119,014
FILING DATE: 1998-07-20
APPLICATION NUMBER: PCT/JP97/04259
FILING DATE: 1997-11-21
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Pred. No. 0.0069;
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                                                                                                                                   US-10-283-349-49
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                                                         Matches
                                                                                             Query Match
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                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
                                                       Local Similarity
es 10; Conserv
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HANAI, No. US20030096977A1uo
TAKAISU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 232384/95 FILING DATE: 11-SEP-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
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COMPUTER READABLE FORM:
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ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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1 SASSSVSYMH 10
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
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                                                                                                                                                                                                                            LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                                                          STRANDEDNESS: single
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REGISTRATION NUMBER: 25,736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/283,349 FILING DATE: 29-Oct-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
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No. US20030096977A1
                                                           Conservative
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IIDA, Akihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1155
                                                                           100.0%; Score 48; DB 15; 100.0%; Pred. No. 0.0069;
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                                                           Mismatches
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                                                                                                           US-09-865-198-23
                                                                                                                                RESULT 11
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                                          Sequence 23, Application US/09865198
Patent No. US20020103345A1
GENERAL INFORMATION:
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Best Local S
Matches 10
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CURRENT APPLICATION NUMBER: US/09/982,107
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 24
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mouse
-09-976-787-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa
-09-982-107-12
APPLICANT: Mhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
CURRENT FILING UNIMBER: US 09/493,539
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR
FILE REFERENCE: 11245/46505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HIATT, ANDREW C. APPLICANT: HEIN, MICH B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/117,726 PRIOR FILING DATE: 1999-01-29
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ORGANISM: Unknown Organism
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US20020159958A1
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; ORGANISM: Mouse
US-09-798-689-8
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US-09-798-689-8
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Sequence 76, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That
TITLE OF INVENTION: Botulinum Neurotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 11245/47102
CURRENT FILING NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 23
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Best Local Similarity
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SEQ ID NO 8
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Matches 10; Conserv
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CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/401,163
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PRIOR FILING DATE: 1997-11--
PRIOR APPLICATION NUMBER: 01
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ORGANISM: Mouse
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ilarity 100.0%;
Conservative 0
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Pred. No. 0.078;
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Pred. No. 0.078;
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Neutralize

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APPLICANT: Ames D
APPLICANT: Ames D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FALING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 82
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
OTHER INFORMATION: 1E8 region VL epitope 1
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US-09-144-886-83
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                                                       TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500, 117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 83
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CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 76
LENGTH: 107
                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
                                                                                                                                                                                                                                                                                                Sequence 83, Application US/09144886 Patent No. US20020155114A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 48; DB 10; Length 107; Best Local Similarity 100.0%; Pred. No. 0.079;
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Best Local Similarity
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                      LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            24 SASSSVSYMH 33
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                                                                                                           ; FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 1G7 region VL epitope 1
US-09-144-886-83
                                                                  Query Match
Best Local Similarity
                                                       Matches
24 SASSSVSYMH 33
                                                       10;
                           1 SASSSVSYMH 10
                                                    100.0%;
nilarity 100.0%;
Conservative 0
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                                                                  Score 48; DB 10;
Pred. No. 0.079;
                                                       Mismatches
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Search completed: July 30, 2003, 10:20:29 Job time: 13.2924 secs

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Minimum
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No.
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                                                                                                                                                                                                                                                                             Match
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Gapop 10.0 , Gapext 0.5
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31
                                      100.0
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:
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     AAW41383
AAW73170
AAY28391
AAY297233
AAB10005
AAB13141
AAB82707
AAB82707
AAB81968
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CDR2 of light chai CDR2 of light chai Peptide fragment f Complementary dete H. pylori 26 kDa p Humanised antibody VEGF antagonist an Ganglioside GD2 sp Mouse ganglioside
                                                                                                                                                                                                                                                                                             Description
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4.5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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108	108	108	108	108	108	108	108	108	107	107	107	107	107	107	107	106	106	106	105	102	102	100	100	100	93	92	60	55	55	œ	7	7	7	7	7
21	21	21	21	21	18	16	13	13	22	22	22	18	18	18	18	24	23	22	17	24	22	17	17	11	23	20	24	24	24	23	24	23	23	23	22
AAY59306	AAY53591	AAY90815	AAB10021	AAY97236	AAW41388	AAR79884	AAR21290	AAR21294	AAG63987	AAB83167	AAB83159	AAW41390	AAW41401	AAW41400	AAW41397	ABJ26730	AAU74418	AAE13144	AAW03182	ABG72734	AAB62264	AAR99876	AAW14487	AAR07319	ABP02151	AAW89175	ABU56883	ABU56882	ABU56871	AAG80315	ABJ26722	AAU74410	AAU81254	AAE25953	AAG63992
DC8 light chain va		.doma VI	H. pylori 26 kDa p	Variable light cha	Anti-CEA antibody		e VL kappa	ş	Amino acid sequenc	Ganglioside GM2 an	Mouse ganglioside	Anti-CEA antibody	Humanised antibody	Humanised antibody	Anti-CEA antibody	VEGF binding relat	Antigen-binding pr	Humanised antibody	Guy's 13 anti-Stre		Light chain constr	Monoclonal antibod	Monoclonal antibod	റ	ORFX p	Σ3. π		HC	AHCb	-human TN	binding	chain	e trk(Mouse anti-KDR p1C	Complementarity de

ALIGNMENTS

RESULT 1 AAW41383

Anti-carcinoembryonic antigen antibody 806.077 diagnosis and therapy of cancer 14-FEB-1997; 04-MAY-1996; 29-APR-1997; Synthetic. WPI; 1997-558987/51. Copley 13-NOV-1997 W09742329-A1 (ZENE) ZENECA LTD. . ය Edge MD, 97GB-0003103. 96GB-0009405. 97WO-GB01165 Emery Ab - used for

Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy; cancer diagnosis; complementarity determining region; light chain.

CDR2 of light chain of anti-CEA antibody.

02-JUN-1998 (first entry)

AAW41383;

AAW41383 standard; peptide; 7 AA

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STSNLAS

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RESULT 2
AAW73170
                                                                                      Query Match
Best Local (
                                                                    Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                      antibody and as a
                                                                                                                                                                                This sequence represents a complementarity determining region (CDR) from the heavy chain of the antibody of the invention. The antibody of the invention is a human CDR transplanted antibody, that reacts specifically with ganglioside GM2. DNA encoding the antibody, and vectors and transformants containing it, can be used for the recombinant production of the antibody. The antibody itself can be used as an anti-tumour agent or as a diagnostic tool for related cancers. The antibody has antitumour activity against ganglioside GM2 positive cells.
                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                    A human type complementarity determining region transplanted antibody against ganglioside GM2 - useful as an anti-tumour and as a diagnostic for related cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-575904/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-tumour agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ganglioside GM2; antibody; complementarity determining region; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDR2 of light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW73170 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 196; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer therapy, seleused for in vivo or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy, selectively killing tumour cells. The antibody can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the light chain of the antibody of the invention. The antil anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK
                                                                Similarity 7; Conserv
STSNLAS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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                                                                                                                                                                                                                                                                                                                                                                                Page 29; 66pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STSNLAS 7
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                                                                100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complementarity determining region
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                                                              Score 31; DB 17;
Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 18;
Pred. No. 9.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          targeting antibody.
                                                                                                                                                                                                          the recombinant production used as an anti-tumour agent The antibody has antitumour
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                                                                                                     Length 7;
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                                                                  Indels
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                                                              Gaps
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RESULT 4
AAY97233
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AAY28391
ID AAY2
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                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                               Sequence
Immunoglobulin; antibody; complementary determing region;
VBGF; vascular endothelial growth factor; KDR;
                                         Complementary
                                                                                              AAY97233;
                                                                                                                    AAY97233 standard; Protein; 7
                                                                                                                                                                                                                                                                                                                          antibodies.
                                                                                                                                                                                                                                                                                                                                                immunoglobulin production.
The chimeric human antibodies have a prolonged half-life and
                                                                                                                                                                                                                                                                                                                                                                            Chimeric human antibodies of the invention are useful in the treatment of cancer, especially that which is of neural ectodermal origin. In contrast to prior art constructs based on mouse monoclonal antibodies, the chimeric human antibodies do not cause anti-mouse anti-mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences AAY28390 DNA and they produce AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Column 157; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric human antibody expression vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody; REI; complementarity determining region; CDR;
chimeric; light chain; heavy chain.
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                                                                                                                                                                                                                                                                                                                                     frequency of adverse effects when
                                                                                                                                                                                                                                                                                                                                                                                                                                  chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                         STSNLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hasegawa M,
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                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                      determining region (CDRL2) of anti-SI(KDR)
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0483528.
93US-0116778.
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                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             90 to AAY28392 replace the CDR regions AAY28394, the hKM796L human anti-GM2 \epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koike M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human anti-GM2 light chain in
                                                                                                                                                                                                                                             <u>.</u>.
                                                                                                                                                                                                                                                        Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        À
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuwana
                                                                                                                                                                                                                                                                                                                                    e a prolonged half-life and a compared to mouse monoclonal
                                                                                                                                                                                                                                                     ) DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakamura
                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                    Length
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                                         antibody.
             CDR
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                                                                                                                                                                                                                                                                                                                                                  reduced
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kinase rinsert domain containing receptor; multivalent; monovalent;

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RESULT 5
AAB10005
ID AAB1
XX
AAB100
XX
AAB10
AC
AB1
XX
DT 01-N
XX
DE H. p
XX
KW Acid
KW Acid
KW Mono
KW Mono
KW CDR
XX
XX
ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc domain-containing receptor (KDR) with a comparable affinity to human CC vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single CC chain antibody, a monovalent single chain antibody, a diabody, a CC triabody, a humanised antibody or a chimerised antibody, a CC triabody, a monovalent single chain antibody, a CC The immunoglobulin molecules bind specifically to an CC vertracellular domain of the KDR receptor with the same affinity as CC VEGF. Overexpression of VEGF has been implicated in a number of the mangioblastoma, central nervous system meoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a CC immunoglobulins of the invention.

CC immunoglobulins of the invention.
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     Unidentified
                                                                                        monoclonal
                                                                                                                                                                                                                             01-NOV-2000
                                                                                                                                                                                                                                                                                        AAB10005
                                                                                                                                                                                                                                                                                                                                             AAB10005 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 50; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-1999;
29-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acquired immune deficiency syndrome; AIDS; human.
                                                                                                                Acid-resistant microorganism; detection; faecal; intestine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                     pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ដ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reduce tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA53765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STSNLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STSNLAS 7
                                                                                                                                                                          26
                                                                                     antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
Ķ
                                                                                                                                                                     kDa protein-binding antibody light chain CDR2 peptide.
                                                                                                                                                                                                                             (first entry)
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99US-0240736.
                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; (
100.0%; (
tive 0;
                                                                                     light
                                                                                  chain; complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 21;
Pred. No. 9.3e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                     determining
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                                                                                     region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC fragments or derivatives) or aptamers (collectively (I)) and detecting (formation of a complex (C) between (I) and the corresponding antigen of (A). The first and second (I) bind to epitopes of different antigens of (Ag). These epitopes are present, after passage through the intestines, (C) in at least some mammals, and have either: (i) their native structure; (C) or (ii) a structure against which an antibody is produced by an animal confected or immunized with (A), or its extract, lysate, derived protein or fragment, or with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect (infection by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, (C) Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, (C) Mycobacterium and campylobacter and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This sequence represents a fragment of a H. pylori 26 kDa protein-binding cused to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
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   Mus
                                                        Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain hypervariable region; VL; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.
                                                                                                                                                                                                                                                                                                                                   AAE13141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-1998;
06-NOV-1998;
                                                                                                                                                                                                               Humanised
                                                                                                                                                                                                                                                                          28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                           AAE13141 standard; peptide; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection by an acid-resistant microorganism (A) by treating a sample with at least two different monoclonal antibodies (MAb)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method for the detection of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 24; Page 21; 84pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA40161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSNLAS
                                                                                                                                                                                                               antibody murine light chain hypervariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cullmann G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA;
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                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98EP-0120687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 21;
Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heppner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                  CDR2.
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RESULT 7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody murine light chain hypervariable region (VI) CDR-2 used in the
02-AUG-2001.
                            WO200154723-A1
                                                         Chimeric - Mus
Chimeric - Homo
                                                                                                                    glioblastoma multiforme; melanoma; therapy; light chain; CDR;
                                                                                                                                                             IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
vascular endothelial growth factor; angiogenesis; antiangiogenic;
antitumour; neoplasm; collagen-vascular disease; autoimmune disea
                                                                                                                                                                                                                             VEGF antagonist antibody IMC-1C11 VL CDR-2.
                                                                                                                                                                                                                                                           15-OCT-2001
                                                                                                                                                                                                                                                                                         AAB82707;
                                                                                                                                                                                                                                                                                                                    AAB82707 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                     complementarity
                                                                                                                                                  tumour; breast carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 15; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD21667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Witte L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US10504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-662942/76.
                                                                                                                                carcinoma; ovarian carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  STSNLAS
                                                                                                                                                                                                                                                                                                                                                                                                                               STSNLAS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rafii S;
                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                        (first entry)
                                                                         ďs.
                                                         sapiens.
                                                                                                    determining
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                                                                                                                                                                                                                                                                                                                        7
                                                                                                  region
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 22;
Pred. No. 9.3e+05;
                                                                                                                                carcinoma; prostate carcinoma; noma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The method
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RESULT 8
AAB81968
ID AAB8
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma, colon carcinoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 of the light chain variable region (see also AAB82702) of IMC-1C11, a mouse human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antipode transport of it, can be used as an anti-angiogenic molecular together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering anti-angiogenic molecule and a chemotherapeutic agent, to produce the second of treating or controlling an angiogenic dependent condition by administering anti-angiogenic molecule and a chemotherapeutic agent, to produce the second of the second of treating or controlling an angiogenic dependent condition by administering anti-angiogenic molecule and a chemotherapeutic agent, to produce the second of the second o
                        29-SEP-2000; 2000WO-JP06773.
                                                                                                                                                                                                                                 Ganglioside; GD2; complementation determining region; CDR; antibody; mouse; cancer.
                                                                                                                                                                                                                                                                                                            Ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating or controlling an angiogenic dependent condition (e.g neoplasm, collagen-vascular or autoimmune disease) in mammal ladministering a combination of an antiangiogenic molecule and
                                                                           05-APR-2001
                                                                                                                            WO200123573-A1
                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    AAB81968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB81968 standard; Peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemotherapeutic agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUNN-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of complementarity determining of the light chain variable region (see also AAB82702) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conserv
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                                                                                                                                                                                                                                                                                                            GD2 specific antibody related peptide SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 37; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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2000US-0539692.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an antibody, which can react specifically with ganglioside GD2, and is transplanted with a human type complementation-determining domain (CDR), or its fragments. The antibody and its derivatives are useful in diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a peptide used in the exemplification of the invention.
                      The present invention relates to derivatives of an antibody against ganglioside GM2. The antibody may be a monoclonal antibody or its fragments. The antibody is combined with a radioactive isotope, protein or small drug in the treatment and diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human type complementation-determining domain transplanted antibody and derivatives against ganglioside GD2, useful in diagnosis and therapy of e.g. tumours, has low antigenicity, little side effects but potent
                                                                                                       radioisotopes
                                                                                                                                           WPI; 2001-266142/27.
                                                                                                                                                                Hanai N,
                                                                                                                                                                                                               30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                 Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                    Mouse ganglioside
                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB83164 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity in cancer
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                                                                                                                   Monoclonal antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100 7; Conservative
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                                                                                Page 72;
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                                                                                                                                                                Nakamura
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                                                                                                                                                                                                               99JP-0278292.
                                                                                                      proteins for treatment and diagnosis of car
                                                                                                                                                                                                                                                                                                                                                                    GM2 antibody light chain variable region CDR2.
                                                                             80pp; Japanese
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100.0%; Pr/
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Pred. No.
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Best Local
                                                Matches
                                                           Query Match
Best Local
                                                                                                                                                                        of the light chain variable region of murine monoclonal antibody 2C4 This antibody binds to human sialoadhesin factor-2 (SAP-2). The antibody is useful for treating or preventing allergic rhinitis, allergies, asthma, anemia, eczema or diseases such as lymphoma, leukemia or systemic mastocytosis in a mammal. It is also useful for
                                                                                                                                 detecting the presence of a cell, especially eosinophil in a sample, by detecting binding of the antibody to SAF-2. The antibody can be coupled to toxins, antiproliferative drugs or radionuclides to
                                                                                                                                                                                                                                                                                     Novel monoclonal antibody specific for human sialoadhesin factor-2 for diagnosis, prevention, treatment of allergy, asthma, eczema or diseases such as lymphoma, leukemia or systemic mastocytosis, in a mammal -
                                                                                                Sequence
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                                                                                                                       kill cells in areas of excessive SAF-2 expression.
                                                                                                                                                                                                                                       AAG63991-93 represent the complementarity determining regions (CDRs)
                                                                                                                                                                                                                                                               Claim 10; Page 34; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Schleimer R;
                                                                                                                                                                                                                                                                                                                                                                               Abrahamson JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2000; 2000US-0187595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-2001; 2001WO-US07193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
leukemia; eosinophil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity determining region of light chain of antibody 2C4
                                                                                                                                                                                                                                                                                                                                           2001-570749/64
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SMITHKLINE BEECHAM
UNIV JOHNS HOPKINS
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                                                Conservative
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                                                           Score 31;
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Pred. No.
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                                                           DB 22;
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RESULT 11 AAE25953

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RESULT 12
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Matches 7
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             Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody; trkA; cisplatin-induced neuropathy; pyridoxine-induced neuropathy; peripheral neuropathy; diabetic neuropathy; neurodegenerative disease; large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;
                                                                                Murine trkC
                                                                                                         09-APR-2002
                                                                                                                                                            AAU81254 standard;
                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                         to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLR)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGP) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR plCl1 scFv antibody light chain complementarity determining region 2 (CDRL2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; immunoglobulin; kinase insert domain-containing receptor; KDI
liver kinase; FLK-1 receptor; vascular endothelial growth fac
tumour growth; light chain complementarity determining region
; anglogenesis; plCl1; scFv antibody.
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WITTE L.
                                                                                                                                                                                                                                                                               Similarity 7; Conser
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                                                                                                                                                                                                                                                                                                                                    7
                                                                               antibody
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                                                                              chain CDR2 of variable region
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Pred. No.
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ches 0;
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eosinopaenia; wound;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an anti-trkC agonist monoclonal antibody which shows no significant cross-reactivity with trkA or trkB, and recognizes an epitope in domain 5 of trkC. The antibodies of the invention are effective in the treatment of cisplatin- or pyridoxine-induced neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre sensory neuropathy, neurodegenerative disease including amyoriphic lateral sclerosis, nerve cell injuries, disorders of insufficient blood cells such as leukopaenia including eosinopaenia, basopaenia, leading the cells such as leukopaenia including eosinopaenia, basopaenia, leading the cells such as leukopaenia including eosinopaenia, basopaenia, leading the cells such as leukopaenia including eosinopaenia, basopaenia, leading the cells such as leukopaenia including eosinopaenia, basopaenia, leading the cells such as leukopaenia including eosinopaenia, basopaenia, leading the cells such as leukopaenia including eosinopaenia, basopaenia, leading the cells such as leukopaenia including eosinopaenia, basopaenia, leading the cells such as leukopaenia including eosinopaenia, basopaenia, leading the cells such as leukopaenia including eosinopaenia, basopaenia, leading the cells such as leukopaenia including eosinopaenia, basopaenia, leading the cells such as leukopaenia including eosinopaenia basopaenia.
                                                                                  Complementarity determining region; CDR; CDRL2; antigen; cytostatic; angiogenesis inhibitor; vascular endothelial growth factor receptor; VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
                                                                                                                                                                                                                                                                                                             AAU74410 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ischaemia and cerebrovascular disorders and in the diagnosis of diseases involving cellular degeneration. Sequences AAU81229-AAU81284 represent human and mouse anti-trkC agonist monoclonal antibodies and antibody fragments of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkinson's disease, Huntington's disease and tumours. The sequences also useful for inducing angiogenesis for treating wounds, ulders and diabetic complications of sickle cell disease, for treating cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel anti-trkC agonist monoclonal antibody useful for treating neurodegenerative disease, shows no significant cross-reactivity with trkA/trkB, and recognizes epitope in domain 5 of trkC -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             basopaenia; lymphopaenia; monocytopaenia; neutropaenia; cancer; ulcer; Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes; sickle cell disease; cardiac ischaemia; cerebrovascular disorder; cellular degeneration; gene therapy.
                                                                  ant ibody
                                                                                                                                                                           Light chain
                                                                                                                                                                                                                        26-MAR-2002
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05-OCT-2000;
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2000US-238319P.
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Pred. No.
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Mismatches 0;
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                 WO2003002144-A1
                                                                                       bispecific
                                                                                                  Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour;
                                                                                                                                                              VEGF binding related peptide
                                                                                                                                                                                                     01-MAY-2003
                                                                                                                                                                                                                                                                          ABJ26722 standard; Peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 55; Page 57; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bispecific immunoglobulin-like antigen-binding protein tumour growth and for inhibiting angiogenesis, comprises a two polypeptides and two second polypeptides -
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                                                                                     cell; vascular er
antigen-binding
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                                                                                       protein;
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RESULT 15
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New bispecific antibodies having antigen-binding sites specific for first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia
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                                                                                                                                                                                                                                TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR; heavy chain; light chain; complementarity determining region; vasot antiarthritic; neuroprotective; protozoacide; toxic shock syndrome; rheumatoid arthritis; malaria; multiple sclerosis.
                                                                                                                                                                                                                                                                                                      Anti-human TNF-alpha CDR-L2 peptide
                                                                                                                                                                                                                                                                                                                                                            AAG80315;
                                                                                                                                                                                                                                                                                                                                                                                      AAG80315 standard; peptide; 8 AA.
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                                     Fukuda Y, Nagahira K,
                                                                                            19-APR-2000; 2000JP-0117394
                                                                                                                      18-APR-2001; 2001WO-JP03308.
                                                                                                                                                   25-OCT-2001.
                                                                                                                                                                                                                                                                                                                                 18-FEB-2002 (first entry)
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                                      Nakanishi
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Pred. No. 9.3
0; Mismatches
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WPI; 2002-066345/09

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Query Match
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Matches 7; Conserv
                                                                                                                                                                                                                                                       This invention describes novel heavy chain and light chain polypeptides or their fragments of a recombinant antibody to human TNF-alpha which contain complementarity determining region (CDR) sequences. The products of the invention have vasotropic, antiarthritic, neuroprotective and protozoacide activity. The antibodies act by neutralising TNF-alpha in vivo. The antibodies are used for producing chimeric and humanised antibodies that may be used for the treatment and prevention of TNF-alpha ancisociated diseases such as toxic shock syndrome, rheumatoid arthritis, malaria and multiple sclerosis. The antibodies have low immunogenicity in humans. This sequence represents the anti-human tumour necrosis factor-alpha (TNF-alpha) light chain CDR1 designated CDR-I2.
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3b; Page 26; 36pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel heavy and light-chain polypeptides of chimeric and humanised antibodies against human tumour necrosis factor alpha for low-immunogenicity treatment of TNF-related diseases such as toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shock syndrome
                                                                                                                                                                                       8 AA;
100.0%; Score 31; DB 23; Length 8; illarity 100.0%; Pred. No. 9.3e+05; Conservative 0; Mismatches 0; Indels
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Search completed: July 30, 2003, 09:36:47 Job time: 8 secs

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> 0; Gaps

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Minimum DB Maximum DB Result No. Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s Title: Perfect score: Database Total number of hits satisfying chosen parameters: Scoring table: Sequence: Run on: OM protein -Searched: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Score seq length: 0
seq length: 2000000000 protein search, using sw model Query Match Length PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* July 30, 2003, 09:31:34; Search time 2.06977 Seconds (without alignments) 325.245 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-865-198-5 31 283308 seqs, 96168682 residues 100.0 STSNLAS 7 Copyright GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd BB \$17626 \$17620 \$17640 \$17640 \$17642 \$17642 \$13730 \$141058 \$141059 \$1410 Ä summaries SUMMARIES Ig kappa chain V r
Ig light chain V r
Ig kappa chain protein neu
probable membrane
Ig heavy chain V r
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Ig heavy chain V r
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Qу	Query Ma Best Loo Matches	RESULT 2 S17630 Ig kappa chain V regio C;Species: Mus musculu C;Date: 22-Nov-1993 #s C;Accession: S17630 R;Clackson, T.; Hoogen Nature 352, 624-628, 1 A;Title: Making antibo A;Reference number: S1 A;Accession: S17630 A;Status: preliminary A;Molecule type: nucle A;Residues: 1-91 cCLA> C;Superfamily: immunog C;Keywordds: heterotetr F;8-81/Domain: immunog	Query Ma Best Loo Matches Qy	33 27 34 27 35 27 36 27 37 27 38 27 39 27 40 27 41 27 42 27 44 2 27 43 27 44 2 27 43 27 45 27 46 27 47 27 48 27 49 27 40 27 40 27 41 27 42 27 43 27 44 27 47 27	3 3 3 1 0
1 STS 41 STS	atch cal Simi 7;	chain V region Wis musculus 2-Nov-1993 #se on: \$17630 n, T.; Hoogenb Making antibod ce number: \$17 on: \$17630 preliminary e type: nuclei s: 1-91 <cla> mily: immunogl s: heterotetra main: immunogl</cla>	atch cal Simi 7; 1 STS	ee: 'persung 4	1 7 8
STSNLAS 7	llarity Conservat	in V region - mounts musculus flous. ov-193 #sequence. \$17630 T.; Hoogenboom, H. 624-628, 1931 ing antibody frag. number: \$17230; M. \$217630 reliminary ype: nucleic acid. 1-91 cCLA- y: immunoglobulin heterotetramer; in: n: immunoglobulin	imilarity ; Conservat STSNLAS 7 STSNLAS 47	11 11 11 11 11 11 11 11 11 11 11 11 11	90.3 13 37.1
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	0%; Score 31; DB 2; 0%; Pred. No. 2.3; 0; Mismatches 0	mouse) evision 10-Nov-1995 .; Griffiths, A.D.; nts using phage disp D:91326098; PMID:190 D:91326098; Immunoglobu umoglobulin omology <imm></imm>	%; Score 31; DB 2; %; Pred. No. 2.3; 0; Mismatches 0	\$68152 \$68152 \$26459 \$226459 \$226459 \$226459 \$226339 \$17624 \$17623 \$17632 \$17633 \$17634 \$17635 \$17636 \$1763	
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R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G. Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries. A;Reference number: S17230; MUID:91326098; PMID:1907718
A;Accession: S17641
                                                                     A; Molecule type: nucleic acid
A; Residues: 1-93 <CLA>
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A;Molecule type: nucleic acid
A;Residues: 1-93 <CLA>
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A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
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C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S17640
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A; Residues: 1-93 <CLA>
A; Residues: 1-93 <CLA>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 8-83/Domain: immunoglobulin homology <IMM>
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                                          C; Superfamily: immunoglobulin V region; immunoglobulin homology
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C.Species: Mus musculus (house mouse)
C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
                                                                                                                    A;Statug: preliminary
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Best Local Similarity
Matches 7; Conserv
                        Keywords: heterotetramer;
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Best Local
-83/Domain: immunoglobulin homology <IMM>
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Ig kappa chain V region (6A7) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 30-Aug-1991 #sequence_revision 30-Aug-19 C;Accession: D38601 R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
                                                                                                         RESULT 8
D38601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unlika; A;Reference number: A33730; MUID:89367325; PMID:2505260
A;Accession: C33730
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A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
A;Accession: S17642
A;Accession: S17642
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C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S17642
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A;Residues: 1-93 <CLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                  F;16-91/Domain: immunoglobulin homology <IMM>
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A;Note: the authors translated the codon TTG for residue 34 as Phe*
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A;Residues: 1-96 <LAW>
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C;Accession: C33730
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tive 0; Mismatches
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C;Superramaty. C;Keywords: heterotetramer; immunogrobulin homology <IMM> F;8-81/Domain: immunoglobulin homology <IMM>
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J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective BA;Reference number: PH0971; MUID:92381444; PMID:1512540
                                                                                                                                                                                                                                                                                                                                                                    Ig light chain V region (clone 17s-c1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1059
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R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol Chem. 266, 2134-2142, 1991
A;Title Common structural features among monoclonal antibodies binding the same antiger A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: D38601
δ
                                                                                                                                          A; Experimental source: B cell, strain [1 C; Superfamily: immunoglobulin V region; C; Keywords: immunoglobulin
                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-99 <TIL>
                                                                                                                                                                                                                                            A;Reference number: PH0971; MUID:92381444; A;Accession: PH1059
A;Status: nucleic acid sequence not shown
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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A; Residues: 1-99 <TIL>
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A;Accession: PH1058
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A; Residues: 1-99 <GOS>
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                                      100.0%; Score 31; DB llarity 100.0%; Pred. No. 2.5; Conservative 0; Mismatches
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A;Molecule type: DNA
A;Residues: 1-109 <BEH>
A;Residues: 1munoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
A;Molecule type: DNA
A;Residues: 1-109 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi A;Reference number: PT0376; MUID:91147903; PMID:1900082
A;Accession: PT0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig light chain V region (S107/VH11 group 3-23) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: PT0404
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J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1060
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                                                                                                   C;Accession: PT0405
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded A;Reference number: PT0376; MUID:91147903; PMID:1900082
A;Accession: PT0405
                                                                                                                                                                                                                            Ig light chain V region (S107/VH11 group 3-38) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Decies: Mo-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999 C;Accession: PT0405
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A; Residues: 1-99 <TIL>
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100.0%; Pred. No. 2.
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A;Title: Immunoglobulin kappa light chain variable region gene complex organization and A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: A32513
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A; Residues: 1-130 < KOF>
A; Residues: 1-130 < KOF>
A; Cross-references: GB: M20834; NID: g196943; PIDN: AAA38846.1; PID: g196944
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer;
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C;Species: Mus musculus (house mouse)
C;Stecie: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
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C.Species: Mus musculus (house mouse)
C.Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
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;23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
;38-111/Domain: immunoglobulin homology <IMM>
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                  SEQUENCE FROM N.A., AND FUNCTION.
MEDLING=20437773; PubMed=10982411;
Kunitomo H., Higuchi T., Iino Y., Yamamoto M.;
"A zinc-finger protein, Ret2p, regulates transcription of the fission yeast stell(+) gene, which encodes a pivotal transcription factor for sexual development.";
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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MEDLINE=92407963; PubMed=1236639;

Chan S.P., Birgit H., Delius H.

"Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and 28 subtypes are all the second secon
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PRINTS; PR00865; HPVCAPSIDL1.
ProDom; PD000544; PV_capsid_L1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; K02718; AAA46943.1; -. EMBL; M96285; AAA47024.1; -. EMBL; A06331; CAA00546.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last annotation update) Major capsid protein L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-85246220; PubMed=2990099;
Seedorf K., Krammer G., Durst M.,
"Human papillomavirus type 16 DNA
Virology 145:181-185(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papillomavirus.
NCBI_TaxID=1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Virol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virol. 66:5714-5725(1992).
MISCELLANEOUS: HPV16, IN COMPARISON TO HPV TYPES 6 AND 11,
OFTEN ASSOCIATED WITH MALIGNANT GENITAL CANCERS IN HUMANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANLAS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STSNLAS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
11:3205-3217 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.3%;
                                                                                                                                                                                                                                                        Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB
Pred. No. 33;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5B3402587093B380 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stage; Papillomaviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ā
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RA SGOUTOS J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser, A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgsom G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagell K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V. Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RN Nature 415:871-880(2002).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE 578A1N=972;
MEDLINE=21848401; F
MOOD V., Gwilliam F
MOOD V., Gwilliam F
                                                            EMBL; AB025941; BAA89273.1; -.
EMBL; Z9853; CAB11086.1; -.
EMBL; D89221; BAA13882.1; -.
EMBL; AB027851; BAA87155.1; -.
EMBL; T11653; T11653.
                                                                                                                                                                                                                                                                                                                                                                                                                 "Large-scale screening of intracellular protein localization is fission yeast cells by the use of a GFP-fusion genomic DNA lib Genes Cells 5:169-190(2000).

-I- FUNCTION: Key transcription factor for sexual development. Activates the transcription of stell. Binds to a stress relement-like (SRE) region in the stell promoter.

-I- SUBCELLULAR LOCATION: Nuclear (Probable).
                     ProDom; PD00000;
SMART; SM00355;
                                                                                                                                                                                                                                            entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                          Pfam; PF00096; zf-C2H2;
                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hiraoka Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20223868; PubMed=10759889; Ding D.-Q., Tomita Y., Yamamoto A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=968 h90
                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 2 C2H2-type zinc fingers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNAs.
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"Identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98162722;
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                         PD000003; Zi
SM00355; ZnF
       PS00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; PubMed=9501991;
to K., Nakai K., O
of open reading f
                                        Znf_
ZĪNC_FINGER_C2H2_1; 1.
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                         C2H2;
                                        _C2H2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of intracellular protein localization in living the use of a GFP-fusion genomic DNA library.";
                                                                               C2H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okayama H., Nojima H.; frames in Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chikashige Y., Haraguchi
                                                                                                                                                                                                                                                                   (See http://www.isb-sib/ch/announce,
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S., Basham
                                                                                                                                                                                                                                                                                                    There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                     Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          response
                                                                                                                                                                                                                                                                                                                                         collaboration
Loutstation -
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RESULT 4
YFK5_SCHPO
DRA CCCCCCCCCCTTTA A BARA A BA
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                                                                                                                                                                                                                                                                                                                                    RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown S., Cronin R., Davis P., Feltwell T., Crurcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
Alames K., Jones M., Leather S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
Alames K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Moodward J., Volckaert S., Saunders D., Seeger K., Sharp S.,
RA Rylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Gerent F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Moreno K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
"The genome sequence of Schizosaccharomyces pombe.",
"The genome sequence of Schizosaccharomyces pombe.",
"The genome sequence of Schizosaccharomyces pombe.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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ZN_FING
ZN_FING
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein C167.05 in chromosom SPAC157.05 OR SPAC57A7.01. Schizosaccharomyces pombe (Fission yeast) Eukaryota; Fungi; Ascomycota; Schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50157; ZINC FINGER C2H2 2; 2.
DNA-binding; Nuclear protein; Zinc-finger; Metal-binding; Repeat;
Activator; Transcription regulation.
                                                   EMBL; AL035248; CAA22850.1; -.
                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21848401;
Wood V., Gwilliam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001
28-FEB-2003
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P87132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154
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156
567 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 36, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
1 protein C167.05 in chromosome I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                           CAB08759.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
128
156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetaceae;
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C2H2-TYPE 2.
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Ly96 (Rel. 33, Last sequen
Ly-DEC-1998 (Rel. 37, Last annotation)
Hypothetical 81.2 kDa protation
YUR134C OR J2120.
Saccharomyces accharomyces accharomyces
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Best Local
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P04945;
13-AUG-1987
13-AUG-1987
15-JUL-1999
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YJ9C YE:
P47166;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                 MOUSE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006015; Usp.
InterPro; IPR006016; Usp_dom.
Pfam; PF00582; Usp; 1.
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                                                                    13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last serger
15-JUL-1999 (Rel. 38, Last anno
15 kappa chain V-VI region NQ2
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EMBL; Z49635; CAA89667.1; -.
PIR; S57157; S57157.
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NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
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Submitted (SEP-1995)
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to the EMBL/GenBank/DDBJ databases.
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OILED COIL (POTENTIAL).
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Pfam; PF00047; ig; 1.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1

PROSITE; PS50835; IG LIKE; 1

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SEQUENCE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                 "DNA nucleotide sequence analysis of the PvuII DNA fragment L of genome of insect iridescent virus type 6 reveals a complex clustomultiple tandem, overlapping, and interdigitated repetitive DNA
                                                                                                                                                                                                                    Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                    P18306;
01-NOV-1990
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                                                                            Virology 167:497-506(1988)
                                                                                                                                                     Fischer M.,
                                                                                                                                                       MEDLINE=89073753; PubMed=3201751; Fischer M., Schnitzler P., Scholz
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            Repetitive protein ORF2
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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BY SIMILARITY.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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kappa immunoglobulin genes
26:57-66(1981).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transport protein particle 23 kDa subunit (TRAPP 23 kDa subunit).
TRS23 OR YDR246W OR YDB419.13.
                                                                                                               GO; GO:0030008; C:TRAPP; IDA.
GO; GO:0030808; P:ER to Golgi transport; IMP.
Gram; PF04099; Sybindin; 1.
Transport; Endoplasmic reticulum; Golgi stack.
SEQUENCE 219 AA; 24863 MW; 8B32B1D5FE3846ED CRC64;
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Oliver K., Harris D.,
Submitted (MAY-1995)
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SGD; S0002654; TRS23.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION:
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Pfam; PF01925; DUF81;
                                                                                                                                                                                                                                                           EMBL; U32705; AAC21867.1;
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                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Integral membrane
-!- SIMILARITY: STRONG, TO E.COLI YFCA.
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                TIGR; HI0198;
                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO M.LEPRAE U1177B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole-genome random sequencing
                                                                                                                         RANSMEN
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185
                       2 TSNLAS 7
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TSNLAS 190
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                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein HI0198.
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                                                                                                                                                                                                                                                                                                license agreement
                                                                                                                                                                                                                                                                                             institutions as long as its content is in no way atement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                           87.1%;
                                                                                                                                                                                         Transmembrane; Co
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Pred. No.
                                                                                                                       POTENTIAL.
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RESULT 11 GTSE_HUMAN ID GTSE_HUMAN

STANDARD;

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RX HDLINES 20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagylley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole G.J., COA A.V., Davis J., Dawson E.,
Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Jibert J.G.R., Goward M.E., Graffam D.V., Griffiths M.N.D., Hall C.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd D.M.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Hall R.E., Jange M.C., Kershaw J., Kimberley A.M., King A.,
RA Martyn I.D., Mashreghi Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Mashreghi Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.,
Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.,
A Mcclard G.K., Ingragon I., Steward C.A., Sulston J.E., Swann R.M.,
RA Scott C.E., Spragon I., Steward C.A., Sulston J.E., Swann R.M.,
RA Williams L., Williams S.A., Williamson H., Willmer T.E., Wilming L.,
RA Williams L., Williams S.A., Williamson H., Willmer T.E., Wilming L.,
RA Williams J., Lewis S., Lin S.-P., Loh P., Malaj E., Nyuen T., Pan H.,
RA Koe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
Dorman A., Fang F., Pu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.,
RA Wang O., Wang Y., Wang Z., White J., Williams D., Wu H., Yao Z.,
RA Wang O., Wang Y., Wang Z., White J., Willer N., Minx P.,
RA Wang O., Shault S., Loh P., Hua P., Lua A., Kenton S., Lai H., Lao H.,
RA Koe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.,
RA Wang O., Shault
MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.
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28-FEB-2003
28-FEB-2003
15-SEP-2003
                                                                                                                                                             TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                  Wilkinson P., Boden
Tilahun Y., Wright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
MEDLINE=20432105; PubMed=10974554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
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                                                                                                                                                                                        FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human)
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Primates;
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1 (B99 homolog)
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gene.";
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                                                                                                                                                                                                                                                                                                                                Khan
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      er G.D
N.K.,

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YBO3 YEAST
ID YBO3 YEAST
AC P38073;
DT 01-0CT-1994
DT 01-0CT-1994
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  ROCCOORDED DAC
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                                                                                                                                                                                                                Query Match
Best Local
Saccharomycetales;
NCBI_TaxID=4932;
[1]
                                                                01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequency
16-OCT-2001 (Rel. 40, Last annotat:
Putative 103.4 kDa transcriptional
                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                            Eukaryota; Fungi; Ascomycota;
                                     Saccharomyces
                                               YBR033W OR YBR0318.
                                                                                                                                                                                                                                                                                         GG; GO:0005881; C:cytoplasmic microtubule; NAS.
GC; GO:0006977; P:DNA damage response, induction of cell
GC; GO:000085; P:G2 phase of mitrotic cell cycle; NAS.
GC; GO:0007017; P:microtubule-based process; NAS.
                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  EMBL; AF223408; AAF31459.1;
EMBL; AL031588; CAB38415.1;
EMBL; BC006325; AAH06325.1;
Genew; HGNC:13698; GTSE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                  Microtubules;
                                                                                                                                                                                                                                                                                                                                          GK; Q9NYZ3; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               progression.
SUBCELLULAR LOCATION:
DEVELOPMENTAL STAGE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quiescent cells.
PTM: Phosphorylated in mitosis (By similarity).
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                                                                                                                                                                            STSNLA 6
                                                                                                                                                                                                       6
                                                                                                                                                                                                                Similarity
                                                                                                                                                                 STSNLA 308
                                                                                                                                                                                                                                          259
506
720
                                                                                                                                                                                                       Conservative
                                     cerevisiae
                                                                                                                                                                                                                                                                                 Phosphorylation.
                                                                                                                                                                                                                                            AA;
                                                                                                                STANDARD;
                  Saccharomycetaceae;
                                                                                                                                                                                                                                                      259
506
                                                                                                                                                                                                                                            76614
                                                                                                                                                                                                                100.0%;
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                          (Baker's yeast)
cota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Cytoplasmic.
Expressed in (
                                                                                                                                                                                                                                            MW;
                                                                          sequence up
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Pred. No.
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->
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                                                                                                                                                                                                                                          -> I (IN REF. 1).
-> W (IN REF. 2; CAB384
ACD91CCCD008A89C CRC64;
                                                                                                                                                                                                     Pred. No. 84;
Mismatches
                                                                ion update)
regulatory
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                                                                                                                 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Associated G2/M phase.
                   Saccharomyces
                                                                                                                                                                                                                        1;
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                            Saccharomycetes;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KELC DROME STANDARD; PRT; 1477 AA Q04652; Q04653; Q9VJA2; Q1-FEB-1994 (Rel. 28, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat Ring canal kelch protein [Contains: Kelch s KEL OR CG7210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00463; ZN2 CY6 FUNGAL 1; 1.

PROSITE; PS50048; ZN2_CY6_FUNGAL 2; 1.

Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; Zinc; Metal-binding.

DNA_BIND 56

EN(2) - CYS(6), FUNGAL-TYPE.

SEQUENCE 919 AA; 103396 MW; 18DD2E37A042E246 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001138; Fungi_TrN
Pfam; PF00172; Zn_clus; 1.
SMART; SM00066; GĀL4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X76078; CAA53688.1; -.
EMBL; Z35902; CAA84975.1; -.
FIR; S45889; S45889
SGD; S0000237; YBR033W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified
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MEDLINE=94378725; PubMed=8091864;
    MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celiniker S.E., Holt R.A., E.
Amanatides P.G., Scherer S.E., Li P.W.,
George R.A., Lewis S.E., Richards S., A
                                                                                                                                                                                                                                                                                                                                                             "Kelch encodes
                                                                                                                                                                                                                                                                                                                                                                                                  Xue
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93201592; PubMed=8453663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities
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                                                                                                                                                                  STRAIN=Berkeley;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSUE=Embryo;
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ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Contains 1 Zn(2)-Cys(6) funga
                                                                                                                                                                                                                                                                                    72:681-693(1993)
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                                                                                                                                                                                                                                                                                                                                                     of intercellular bridges in Drosophila egg
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Evans C.A., Gocayne J.D.,
., Hoskins R.A., Galle R.F.,
Ashburner M., Henderson S.N.,
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RA Ballaw R.M., Basu A., AH. N.-V., ANDEWS FIGHLINGOLI C., Bedsley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Glabart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Melson D.R., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Sinpson M., Skupski M.P., Smith T.,
RA Surskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Yellams S.M., Wodsge T., Worley K.C., W.D., Yang S., Yao Q.A.,
RA Yellams S.M., Wolson K.A., Shubin G.M., Venter J.C.,
RT The genome sequence of Drosophila melanogaster.",
Schad C., Schad 
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IISSUE=Embryo;
                                                                                                                            CHARACTERIZATION.
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MEDLINE=97236487; PubMed=9118811;

codon suppression.";
Development 124:1405-1417(1997). Robinson D.N., Cooley L.; "Examination of two kelch proteins generated by stop

- FUNCTION: FUNCTION: COMPONENT OF RING CANALS THAT REGULATES THE FLOW OF CYTOPLASM BETWEEN CELLS. MAY BE INVOLVED IN THE REGULATION OF CYTOPLASM FLOW FROM NURSE CELLS TO THE OOCYTE DURING OOGENESIS
- BINDS ACTIN.
 SUBCELLULAR LOCATION:
 CANALS PRESENT IN EGG INNER SURFACE OF CYTOPLASMIC BRIDGES OR CHAMBERS. SUBCORTICALLY IN IMAGINAL DISK DISK RING
- PPITHELIA.

 -! TISSUE SPECIFICITY: BOTH PROTEINS ARE EXPRESSED IN OVARIES, MITSUE SPECIFICITY: BOTH PROTEINS ARE EXPRESSED IN OVARIES, MITSUES, CUTICLE, SALIVARY GLAND AND INFESTIS, OVARECTOMIZED FEMALES, CUTICLE, SALIVARY GLAND AND INAGINAL DISKS. KELCH ORF1 IS THE PREDOMINANT PROTEIN AND IS EXPRESSED IN FAT BODIES. ON ENTRY INTO METAMORPHOSIS LEVELS COULT LENGTH PROTEIN INCREASE IN TESTIS AND IMAGINAL DISKS.

 -!- DEVELOPMENTAL STAGE: LARVAE, PUPAE AND ADULTS.

 -!- SIMILARITY: Contains 1 BTB/POZ domain.

 -!- SIMILARITY: Contains 6 Kelch repeats.

 -!- SIMILARITY: Contains 6 Kelch repeats.

 -!- CAUTION: Ref. 2 sequence differs from that shown due to errong the second of the second MALE
- erroneous

gene model prediction.

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EMBL; L08483; AP L08483; AP AE003657; AAA53471.1; AAA53472.2;

EMBL; AAF53651.1; ALT_SEQ

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Best Local
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FlyBase; rBgn0001301; kel.
GO; GO:00077292; P:oogenesis; IMP.
GO; GO:0007301; P:ring canal form
InterPro; IPR000210; BTB POZ.
InterPro; IPR006651; Kelch.
InterPro; IPR006652; Kelch.
Pfam; PF00651; BTB; 1.
Pfam; PF00651; BTB; 1.
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Submitted
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                                      This
                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mitochondrial import inner membrane translocase
TIM8 OR YJR135W-A OR YJR135BW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
DOMAIN
REPEAT
   modified
            the
use
                              between
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces.
                                                                                                                                                                                                 P57744;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
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SMART; SM00225; BTB; 1.
SMART; SM00612; Kelch; 6.
PR0SITE; PS50097; BTB; 1.
                                                                                                                           NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoskeleton;
Ween the Swiss Institute or Browner The European Bioinformatics Institute. The by non-profit institutions as long by non-profit institutions as long of the aratement is not removed.
                                                                      mitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Involved in mitcochondrial carrier import.
SUBCELLULAR LOCATION: Mitochondrial inner membrane ()
                                                      SIMILARITY: Belongs to the Tim8/Tim10 family.
                                                                similarity)
                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss_Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                   YEAST
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ilarity 100.0%;
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POLY-GIN.
PORABLE.
V-> A (1)
A-> R (1)
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KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
KELCH 6.
ASN-RICH.
GLN-RICH.
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Pred. No.
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formation;
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BTB.
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                                                                                                                                                                                                                                                                                                 Mismatches
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G (IN REF. 1).
4851EEAE9D9DBA47
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J. 1.9e+02;
O;
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          There are no restrictions ng as its content is in
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RESULT 15
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnston M., Andrews S., Brinkman R., Cooper J., Ding H. Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirı Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Whan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson Vaudin M.
                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (Rel. 15, Creat
01-AUG-1990 (Rel. 15, Last
01-OCT-1996 (Rel. 34, Last
Sporulation protein SPO12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z49636; -; NOT_ANNOTATED_CDS.
PIR; S78075; S78075.
SGD; S0007348; TIMB.
GO; GO:0005758; C:mitochondrial intermembrane GO; GO:0005758; P:mitochondrial translocation; GO; GO:0006628; P:mitochondrial translocation;
                                                                                         or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90258869; PubMed=2188099; Malavasic M.J., Elder R.T.; Malavasic M.J., Elder R.T.; "Complementary transcripts from two genes necessary for normal meiosis in the yeast Saccharomyces cerevisiae."; mol. Cell. Biol. 10:2809-2819(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SP12_YE
P17123;
                                                                                                                                                                                        between the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                              This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
                                                                                                                                                                                                                                                                                       -i- FUNCTION: IT IS REQUIRED FOR SPORULATION.
SPORULATION.
-i- MISCELLANEOUS: ITS NEGATIVE
-i- SIMILARITY: TO YEAST G8558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=S288c / AB972;
MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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Pfam; PF02953; zf-Tim10_DDP; 1.
Transport; Protein transport; Translocation; Mitochondrion;
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                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete nucleotide sequence of
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                   M32653; AAA35076.1;
U10397; AAB68979.1;
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DR SGD; S0001195; SPO12.

DR GO; GO:0005730; C:nucleolus; IDA.

DR GO; GO:0007096; P:exit from mitosis; IGI.

DR GO; GO:0007096; P:exit from mitosis; IGI.

DR GO; GO:0007127; P:melosis I; IMP.

DR GO; GO:0007127; P:melosis I; IMP.

DR GO; GO:0000278; P:mitotic cell cycle; IEP.

DR Pfam; PF05032; SpO12; 1.

KW Sporulation; Melosis.

PT DOMAIN 159 173 AA; 19912 MW; E114394516451F60 CRC64;

SQ SEQUENCE 173 AA; 19912 MW; E114394516451F60 CRC64;

QUERTY MATCH 83.9%; SCOTE 26; DB 1; Length 173;

Best Local Similarity 85.7%; Pred. No. 28;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 STSNLAS 7

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Db 78 STSNLAS 84

Search completed: July 30, 2003, 09:45:06

Job time: 4.09302 secs
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Result
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1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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14 US-10-232-187-9

14 US-10-032-482-4

10 US-09-982-107-12

9 US-09-986-198-23

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Sequence 5, Appli
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APPLICANT: Witte, Larry
ITILE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
NUMBER: WordDerfect 8.0 for Windows
SOFTWARE: WordDerfect 8.0 for Windows
SEQ ID NO 5
LENGTH: 7
TYPE: PRT
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Ü	55,	e 55,	W	e 16,	e 28,	Sequence 16, Appl	13,	13,	2		2	e 27,	,	Sequence 21, Appl	28,	Sequence 29, Appl	99,	97,	æ	17,	equence 113	e 111	equence 89,	e 9,	ев,	Sequence 8, Appli	equence 4, 1	е 88,	Sequence 76, Appl

ALIGNMENTS

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US-09-865-198-5
Sequence 5, Application US/09865198; Patent No. US20020103345A1; GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
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CURRENT FILING DATE:

2001-03-02

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LENGTH: 7
TYPE: PRT
                                                                                                            Sequence 5, Application US/09798689 Publication No. US20030103973A1 GENERAL INFORMATION:
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Matches 7; Conser
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AFFLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. US20020142359A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
PRIOR APPLICATION NUMBER: GB 9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 09/171,945
PRIOR FILING DATE: 1998-10-29
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CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT FILING DATE: 2001-07-23
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APPLICANT: Edge, Michael Derek
APPLICANT: Emery, Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
TITLE OF INVENTION: Their Therapeutic use in an Adept System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
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CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 8.0 for Windows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and MethoTITLE OF INVENTION: Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                4e+05;
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RESULT 5
US-10-195-752-109
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SEQ ID NO 5
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TYPE: PRT
ORGANISM: Mouse
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                                                                                                            INFORMATION FOR SEQ ID NO: 109:
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nes 7; Conserv
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MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/195,752
FILING DATE: 16-Jul-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION UNMEER: US/09/393,385B
FILING DATE: 27-JUN-96
TELECOMMUNICATION INFORMATION:
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
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                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA
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                                                                                                                           TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 22201-4714
                                                                          LENGTH: 7 amino acids
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100.0%; Pred. No. 4e+05;
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US-10-232-187-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/232,187
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/187,595
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: 607/US01/07193
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/315,943
PRIOR APPLICATION NUMBER: 60/315,943
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-30
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Best Local Similarity 100.0%;
Matches 7; Conservative 0
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Publication No. US20020197270A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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SEQ ID NO 9
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               PRIOR APPLICATION NUMBER: US/09/445,602
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: PCT/IL98/00266
                                                                  FILE REFERENCE: COHEN42
CURRENT APPLICATION NUMBER: US/10/032,482
CURRENT FILING DATE: 2002-01-02
                                                                                                                         APPLICANT: HERKEL, Johannes
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Abrahamson, Julie A. APPLICANT: Bochner, Bruce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/394,741 FILING DATE: 2002-07-10
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Erickson-Miller, Connie
Kikly, Kristine K.
                                                                                                                                                                                  RUIZ, Pedro
EREZ-ALON, Neta
                                                                                                                                                                                                                       ROTTER, Varda
Wolkowicz, Roland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schleimer, Robert
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Pred. No. 4e+05;
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Pred. No. 4e+05;
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CURRENT APPLICATION NUMBER: US/09/982,107
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
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                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                          Sequence 24, Application US/09976787 Patent No. US20020064528A1
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Patent No. US20
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     Matches
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APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
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PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HIATT, ANDREW C. APPLICANT: HEIN, MICH B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Unknown Organism
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TYPE: PRT
ORGANISM: Mus musculus
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NAME/KEY: misc feature
LOCATION: (53)..(53)
OTHER INFORMATION: Xaa
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Pred. No.
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Best Local Similarity
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Best Local
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Publication No. US20030103973A1
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                                                                                                                                                                             TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                  SEMERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and MethorITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT EPPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
                                                                                                             PRIOR APPLICATION NUMBER: 08/9
                                                                                                                                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-(
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 PAPPLICATION NUMBER:
                                                APPLICATION NUMBER: FILING DATE: 1995-
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APPLICATION NUMBER:
FILING DATE: 1996-
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08/196,041
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Pred. No.
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Pred. No.
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US-09-910-059-61
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                                                                                                                                                                                                 Sequence 61, Application UPatent No. US20020142359A1
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Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
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CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 09/171,945
PRIOR FILING DATE: 1998-10-29
                                                             APPLICANT: Emery, Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA,
TITLE OF INVENTION: Their Therapeutic use in ar
FILE REFERENCE: 1991-209
                                                                                                                          APPLICANT: Copley, Clive G
APPLICANT: Edge, Michael Derek
APPLICANT: Emery, Stephen Char
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APPLICANT: Edge, Michael Derek
APPLICANT: Emery, Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjug:
TITLE OF INVENTION: Their Therapeutic use in an Adept
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TYPE: PRT
ORGANISM: Mouse
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SOFTWARE: Patentin Ve
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PRIOR FILING DATE: 1997-04-29
PRIOR APPLICATION UNMBER: GB 9703103.3
PRIOR FILING DATE: 1997-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 1991-209
CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT FILING DATE: 2001-07-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: OTHER INFORMATION: humanized light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 1998-10-29
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Pred. No.
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PRIOR APPLICATION NUMBER: PCT/GB97/01165

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; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: INFORMATION: humanised light chain variable region variant
US-09-910-059-61
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US-09-910-059-71
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US-09-910-059-65
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Best Local Similarity
Matches 7; Conserv
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Patent No. US20020142359A1
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Best Local (
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                                                                                     GENERAL
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TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
TITLE OF INVENTION: Their Therapeutic use in an Adept System
FILE REFERENCE: 1991-209
CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT FILING DATE: 2001-07-23
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PRIOR FILING DATE: 1996-05-04
NUMBER OF SEQ ID NOS: 131
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PRIOR FILING DATE: 1997-04-29
PRIOR APPLICATION NUMBER: GB 9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
                                        APPLICANT: Copley, Clive G
APPLICANT: Edge, Michael Derek
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APPLICANT: Edge, Michael Derek
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TYPE: PRT
ORGANISM: Artificial Sequence
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CANT: Emery, Stephen Charles
OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: GB 9703103.3
FILING DATE: 1997-02-14
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                                                                                   INFORMATION:
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                  , OTHER INFORMATION: humanised light chain variable region variant US-09-910-059-71
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR APPLICATION NUMBER: CT/GB97/01165
PRIOR FILING DATE: 1997-04-29
PRIOR APPLICATION NUMBER: GB 9703103.3
PRIOR FILING DATE: 1997-02-14
                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.1
SEQ ID NO 71
                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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EMBL, AF516283; AAM64201.1; -.

InterPro; IPR003399; Ig.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003306; Ig_MHC.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-ORT-2002 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1
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Q26306 drosophila
Q12271 saccharomyc
Q9j176 mus musculu
Q9c5k8 arabidopsis
Q8jmus human papil
Q8jmus human papil
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C STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;
C STRAIN-BALB/c; TIPAGE V., Paulice Propose to the publication of L-VIPase VL domains.";
C STRAIN-BALB/c; TIPAGE V., Paulice Propose to the publication of L-VIPase VL domains.";
C STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;
C TIPAGE V.

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF516284; AAM64202.1;
R InterPro; IPRO03599; Ig.
NR InterPro; IPRO03596; Ig.
NR INTERPRO; IPROPINE INTERPRO; IPROPINE INTERPROPINE INTERP
                                                                                                       Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Rez Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson Haselkorn R., Kyrpides N., Overbeek R.; "The genome sequence of the facultative intracellular path Brucella melitensis.";
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Pfam; PF(
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EWEL; AE009642; AAL53275.1;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=16M / ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar
                                                                                                                                                                                                                                                                                                                                               Brucellaceae; Brucella.
NCBI_TaxID=29459;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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01-MAR-2003 (TYEMBLYE1 23, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
Nus musculus (Mouse)
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Mammalia; Eutheria;
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01-MAY-2000
01-MAY-2000
01-OCT-2002
                                                                                                  Bourg G., Foulongne V., Frutos P., Kulakov Y., Ramuz M.; "A homologue of the Agrobacterium tumefaciens VirB and Bourtussis Ptl type IV secretion systems is essential for survival of Brucella suis.";
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Bacteria; Proteobacteria;
Brucellaceae; Brucella.
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EMBU; AF226278; AAF73903.1; -.
InterPro; IPR005498; TrbI.
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Sieira R., Comerci D.J., Sanchez D.
"A Homologue of an Operon Required
Is Required in Brucella abortus for
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Brucellaceae; Brucella.
Pfam; PF03743;
SEQUENCE 391
                                                          MOl. Microbiol. 33:1210-1220(1999).
EMBL; AF141604; AAD56620.1; -.
                                                                                                                                                                                         MEDLINE=99440171; PubMed=10510235;
O'Callaghan D., Cazevieille C., Al
                                                                                                                                                                                                                                        STRAIN=1330;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         VIRB10
                                                                                                                                                                                                                                                                                                                                                                                                                 VirB10
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Pred. No. 24;
0; Mismatches
A6DCA4C9AFBB490D CRC64;
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red for DNA Transfer in Agrobacterium
for Virulence and Intracellular
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Q37901;
01-NOV-1996
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SEQUENCE
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MEDLINE=22247741; PubMed=12271122;
Pauleen I.T., Seshadri R., Nelson K.E.,
                                                    SEQUENCE FROM N.A.

MEDILINE=96204568; PubMed=8623528;

Mondigler M., Holz T., Heller K.J.;

"Identification of the receptor-binding bacteriophages T5 and BF23.";

Virology 219:19-28(1996).
                                                                                                                                                                                                                                                                                          Bacteriophage BF23.
Viruses; dsDNA viruses,
T5-like viruses.
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Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
EMBL; AE014510; AAN33272.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson M.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S. Nelson W.C., Tettelin H., Gill S.R., White O., Salzberg S.L., Halling S.M., Boyle S.M., Fraser C.M.; "The Brucella suis genome reveals fundamental similarities between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=29461;
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                     Virology 219:1
EMBL; L42820;
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    23, Last sequence update)
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CRC64;
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RESULT 9
Q12271
ID Q1222
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DT 01--V
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Q26306
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InterPro; IPR001841; Znf_ring.
Pfam; PR00097; zf-C3HC4; 1.
SMART; SM00588; NEUZ; 2.
SMART; SM00184; RING; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Metal-binding; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
01-NOV-1996
01-MAR-2003
                                                                                                                                                                                                                                                                                                                       Q12271; PRELIMINARY;
Q12271; O1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is expressed in precursors of larval EMBO J. 12:2586-2586 (1993).
-- SIMILARITY: CONTAINS 1 RING-TYPE EMBL; S62597; AAB27151.1; -- FlyBase; FBgn0002932; neur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Bukaryota; Bridopterygota; Diptera; Brachycera;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                        Benes V., Andrade M.
Sander C., Valencia
                                                                                                                                                                                                                                                          YOR3231W from chromosome XV.
INP53 OR YOR3231W OR YOR109W.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metal-binding; Zinc SEQUENCE 753 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93285130; PubMed-8508781;
Boulianne G.L., la Concha A., Campos-Ortega J.A., Jan L.Y.,
"The Drosophila neurogenic gene neuralized encodes a novel processed in precursors of larval and adult neurons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q26306
Voss H., Ben
Ansorge W.;
                                                                                      Submitted
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                 Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                        SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI_TaxID=4932;
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23,
                                                                                    Rechmann S., Teodoru (Ansorge W., Voss H.; the EMBL/GenBank/DDBJ
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                      Teodoru C.,
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era; Muscomorpha;
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                      Schwager C.,
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                                                                                                                                 Banrevi
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RESULT 11
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Matches 7
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Q9JL76;
01-OCT-2000
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 1.
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EMBL; AF206030; AAF69328.1; -.
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malkiel S., Liao L., Cunningham M.W., Diamond B.; "T-Cell-dependent antibody response to the dominant streptococcal polysaccharide, N-acetyl-glucosamine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2003
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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PF02383; Syja N; 1.
; SM00128; IPPC; 1.
TE; PS50275; SAC; 1.
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IPR000300; IPPC.
IPR002013; Syja_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (JUL-1996)
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                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         10542 MW;
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Rodentia;
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15, Last sequence update)
23, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                 Score 28;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                         C9EE1FFE1F49DA1C CRC64;
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Sciurognathi;
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RESULT 12
Q8JMUG
Q8JMU
ID Q8JMU
AC Q8JMU
AC Q8JMU
O1-OC
DT 01-OC
DT 01-MA
DE Major
GN L1
OS Human
OC Virus
OC Papil
OX NCBI
RN [1]
RN [1]
RN [1]
RN GTUZ
RP SEQUE
RC STRAI
RA Gruz
RA Marti
RA Cruz
CRA Marti
RA Submin
DR EMBL;
DR Pfam;
DR Pfam;
DR Pfam;
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Best Local
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Q8JMU6;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                           Cruz M.R., Cerqueira D.M., Camara G.N.L., Silv Martins C.R.F.; Martins c.R.F.; Thuman papillomavirus type 16 variants in Cent Submitted (APR-2002) to the EMBL/GenBank/DDBJ EMBL; AY098925; AAM29173.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Jonés T., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jonés T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm G.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length cDNA of gene F22D1.70/AT5g20900."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Strephyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rósidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                              Viruses; dsDNA viruses, Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theologis A.;
"Full Length cDNA of gene F22D1.70/AT5g20900.";
submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical 19.9 kDa protei F22D1.70/AT5G20900.
InterPro; IPR002210; PV_capsid_L1.
Pfam; PF00500; late_protein_L1; 1.
PRINTS; PR00865; HPVCAPSIDLI.
                                                                                                                              STRAIN=Bsb-102;
                                                                                                                                                                                                                            Human papillomavirus type
                                                                                                                                                                                                                                                          Major capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000194; ATPase_a/bcentro
PROSITE; PS00152; ATPASE_ALPHA_BETA;
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Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W.,
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Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J
Carninci A., Karlin-Neumann G., Kawai J., Kim C., Lam B.,
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID=10581;
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
d protein L1 (Fragment).
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                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Pred. No.
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                                                                                                                                                                                                           Papillomaviridae;
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                                                                               in Central Brazil.";
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umi M., Yu G., Bowser
i Y., Ishida J., Jone
                                                                                                                                                                                                                                                                             update)
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                                                                 databases.
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Ecker J.R.,
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RESULT 13
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Q8JMU5
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Best Local S
Matches 6
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Best Local
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NON TER
SEQUENCE
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ProDom;
     SEQUENCE FROM N.A.

STRAIN-BBb-14;
CTUZ M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carva:
Martins C.R.F.;
"Human papillomavirus type 16 variants in Central Brazil.";
Submitted (APP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                   01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Major capsid protein L1
                                                                                                                                                                    Q8JMU5;
01-OCT-2002
                                                                                                                                                                                         SnMred
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY098921; AAM29169.1; -. InterPro; IPR002210; PV_capsid_L1.
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus type 1 Viruses; dsDNA viruses, no
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Major capsid protein L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ОВЛМПЭ
                                                                                Human papillomavirus type 16.
Viruses; dsDNA viruses, no RN.
Papillomavirus.
NCBI_TaxID=10581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Bab-178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10581;
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PRINTS; PR00865; HPVCAPSIDL1.
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                                                                                                                                                                                                                                                                                  Local Similarity tes 6; Conserv
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tted (APR-2002) to the AY098926; AAM29174.1;
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                                                                                                                                                                                                                                                                                                                                                         PD000544; PV_capsid_L1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD000544; PV_capsid_L1; 1.
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208 AA;
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23455 MW; 936AAODDA7EDE483 CRC64;
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23840 MW;
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. 22, Last seq
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1 (Fragment).
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o RNA stage;
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                                                                                                                                                         Last sequence
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Pred. No. 1e+0
1; Mismatches
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1e+02;
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                                        Silva E.O., Carvalho L.G.S.,
                                                                                                                                                        update)
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SEQUENCE
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Seeger K., Murphy L., Harris
Quail M., Barrell B.;
Submitted (SEP-2002) to the
EMBL; AL844506; CAD50798.1;
                                                                                                                                                                                                                            Q8IC42;
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Pfam; PF00500; late_Drotlein_L1; 1.
PRINTS; PR00865; HPVCAPSID11.
ProDom; PD000544; PV_capsid_L1; 1.
                                                                                          Hypothetical SEQUENCE 25
                                                                                                                                                                   Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                                           Hypothetical protein.
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Apicomplexa;
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                                                                   Score 28;
Pred. No.
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Pred. No. 1.1e+02;
                                                                                          0488837CF18651D9 CRC64;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34; Search time 2.25581 Seconds (without alignments)
131.295 Million cell updates/sec

Title: Perfect score: US-09-865-198-5 31

Scoring table:

STSNLAS 7

BLOSUM62 Gapop 10.0 , Gapext 0.5

328717 seqs, 42310858 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*
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/cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	Մ	4	ω	2		Result No.
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Sequence 17, Appl	Patent No. 5455030	•	_	_	37,	Sequence 37, Appl	113,	111,	92,	2	Ņ,	8	9,	Sequence 8, Appli	71,	Sequence 65, Appl	61,	e 50,	æ	e 12,	e 15,	e 109,	e 27,	e 98,	e 10,	n	Description

1 STSNLAS

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Mismatches

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Gaps

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ALIGNMENTS

Query Match Best Local Similarity """ hes 7; Conserve US-08-116-778E-10 RESULT 1 US-08-116-778E-10 Patent No. 5830470 GENERAL INFORMATION: Sequence 10, Application US/08116778E TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
CCANSIFICATION: 424 REFERENCE/DOCKET NUMBER: 24: TELECOMMUNICATION INFORMATION: TELEPHONE: (703)816-4000 APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49 ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32, MOLECULE TYPE: peptide CORRESPONDENCE ADDRESS: STREET: 1100 NOR: CITY: ARLINGTON STATE: VIRGINIA COUNTRY: U.S.A. ZIP: 22201-4714 LENGTH: 7 amino a TYPE: amino acid TOPOLOGY: linear ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD 7 amino acids SHITARA, KENYA HANAI, NOBUO KUWANA, YOSHIHISA NAKAMURA, KAZUYASU KOIKE, MASAMICHI 100.0%; Score 31; DB 2; 100.0%; Pred. No. 2.5e+05; 32,955 10: 249-59 Length 7;

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Patent No.
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                    APPLICANT:
NUMBER OF SEQUENCES:
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SOFTWARE: Patentin Release ". The Patentin Rel
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WILSON, MARY J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 10-MAN CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                       INFORMATION:
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5. 5939532
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1100 NORTH GLEBE ROAD
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                            HASEGAWA, MAMORU
PENTION: HUMANIZED ANTIBODIES
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                                                                                                  KUWANA,
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Pred. No. 2.5e+05;
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                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: GB970
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB960
PRIOR APPLICATION NUMBER: GB960
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/C
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver: 2.1
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Best Local S
Matches 7
                                      Matches
                                                         Query Match
Best Local
                                                                                                                                                                                                                                SEQ ID NO 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/09171945 Patent No. 6277599
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Co
TITLE OF INVENTION: Antibody, and Their Therapeuti
FILE REFERICE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703)816-410
INFORMATION FOR SEQ ID NO:
                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: humanizéd
                                                                                                                                                      FEATURE:
                                                                                                                                                                                                            ENGTH:
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LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-UN-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPTWANDS TO THE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (703)816-4000
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                                                         Similarity
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1100 NORTH GLEBE ROAD
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(703)816-4100
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                        100.0%; Score 31; DB 3; 100.0%; Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                             GB9703103.3
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                                                                                                                                                                                                                                                                                                                                          GB9609405.7
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Pred. No. 2
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US-09-393-385B-109

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Matches 7; Conserv
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COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
""MEDIUM TYPE: IBM PC compatible
                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 64235:
GENERAL INFORMA
                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Bosslet, Klaus
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tetravalent Bispecific Receptors, The
TITLE OF INVENTION: Preparation and Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEPAS: (703)816-4100
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
TITLE OF IN
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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CITY: ARLINGTON
                                                                                                                   STREET: 1300 I St
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                  ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
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40. 5959083
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                                                                                                                                            B: Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 amino acids
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VENTION: HUMANIZED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHITARA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P41
FILING DATE: 03-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kulik, David J.
REGISTRATION NUMBER: 36,57
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                            PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
                                                                                                                                                                             OPERATING SYSTEM: IBM P.C. SOPTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                             APPLICATION NUMBER: 08/30
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOWAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
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                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                              STREET: Suite 470
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01
CLASSIFICATION:
                                                                                                                                  CLASSIFICATION:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                               COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                 633 West Fifth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202-408-4000
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                                                              08/367,395
                                                                                                                                                               US/08/434,000A
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                                                                              including application described below:
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US-09-312-157-12
; Sequence 12, Application
; Patent No. 6303341
; Patent No. 6303341
; GENERAL INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-312-157-12
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Best Local Similarity
Thes 7; Conserve
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ACTERISTICS:
105 amino acids
arps: amino acid
STRANDEDURES; single
TOPOLOGY: linear
TOPOLOGY: nr.
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                                                               INFORMATION FOR SEQUENCE LISTING
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (615) 552-0159
                                                                                                                                                                                                      NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 19
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/434,000 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STSNLAS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                          TELEFAX: (619) 552-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                           TELEX: 67-351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM:
                                  DESCRIPTION:
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Pred. No. 5.8;
0; Mismatches
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                  Guy's 13 Kappa
O: 12:
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APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA,
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR PILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR PILING DATE: 1996-05-04
PRIOR FILING DATE: 1996-05-04
PRIOR FILING DATE: 1996-05-04
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOSTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Emery, Stephen
APPLICANT: Copley, Cilve Graham
APPLICANT: Copley, Cilve Graham
APPLICANT: Copley, Cilve Graham
APPLICANT: Copley, Cilve Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Compising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION UNMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR PILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR PILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
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US-09-171-945-61
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SOFTWARE: Pace
; SEQ ID NO 50
FENGTH: 107
                                             SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local Similarity
Matches 7; Conserv
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LENGTH: 10
TYPE: PRT
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TYPE: PRT
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Pred. No. 5.8;
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ORGANISM: Artificial Sequence

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APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR APPLICATION NUMBER: GB9703103.3
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Best Local Similarity
                                                                              APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR APPLICATION NUMBER: GB9609405.7
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                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
                                     PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
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                   NUMBER OF SEQ ID NOS:
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No. 6277599
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ANT: Emery, Stephen
                                                                                                                                                                                                                                                                                                                       71, Application US/09171945
5. 6277599
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Patentin Ver.
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S: 131
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Pred. No. 6;
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Pred. No. 6;
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US-09-171-945-9

Sequence 9, Application Patent No. 6277599

US/09171945

GENERAL

APPLICANT: APPLICANT: APPLICANT:

INFORMATION:
ANT: Emery, Stephen
ANT: Copley, Clive Graham
ANT: Bdge, Michael Derek

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Patent No. 6054561
                                                       Matches
                                                                   Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                              ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                   ENGTH:
51
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RESULT 15
US-09-343-698-8
; Sequence 8, Application
; Patent No. 6475486
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: humanized -09-171-945-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: GB9-
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System FILE REFERENCE: Monoclonal Antibody to CEA CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR APPLICATION NUMBER: GB9703103.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
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  INFORMATION FOR
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ORGANISM: Artificial Sequence
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                                                                APPLICATION NUMBER: 08/325,955
FILING DATE: <UNKNOWN'S
ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: 05552.0981-04000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/343,698
FILING DATE: 30-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sedlacek, Hans-Harald
TITLE OF INVENTION: Glycosyl-Etoposide Prodrugs, A Process For
Preparation Thereof And The Use Thereof In Combination With
Punctionalized Tumor-Specific Enzyme Conjugates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Seeman, Gerhard
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ADDRESSEB: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
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7; Conserv
TELEPHONE: 202-408-4000

###LEFAX: 202-408-4400

DN FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09343698
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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Kolar, Cenek
Hoffman, Dieter
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Search completed: July 30, 2003, 09:38:30 Job time: 3.25581 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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      S40379
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174K ninac protein
18 kappa chain V r
penicillin-binding
19 kappa chain V r
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Ig kappa chain V r
Ig light chain V r
Ig light chain V r
Ig kappa chain pre
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A; Residues: 1-132 <LEV>
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68.8	68.8	68.8	68.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8
108	108	93	77	653	399	397	380	377	343	341	341	341	341	275	144
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PS0069	K1HUKU	S17635	D30502	·S67035	H84108	B70048	855923	T12042	KHDO	E85690	F90900	C90833	VHBPEL	H82106	PL0106
_	Ig kappa chain V-I	Ig kappa chain V r	Ig kappa chain V r	probable membrane	ABC transporter BH	conserved hypothet	cysteine proteinas	cysteine proteinas	cysteine proteinas	probable capsid pr	probable major cap		major capsid prote	emotaxis pro	Ig kappa chain pre

ALIGNMENTS

Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S17641
R;Clackson, T:; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
A;Accession: S17641
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-93 <CLA> RESULT 2 S17641 C;Keywords: heterotetramer; immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <NG>
F;15-132/Product: Ig kappa chain (fragment) #status predicted <MAY
F;15-108/Domain: V region (V-kappa-1) <VRE>
F;30-103/Domain: immunoglobulin homology <IMM>
F;109-132/Domain: J region (J-kappa-4) (fragment) <JRE> A;Cross-references-_EMEL:X14098; NID:g52562; PIDN:CAA32260.1; PID:g736261
R;Carroll, W.L.; Starnes, CO.; Levy, R.; Levy, S.
J. Exp. Med. 168, 1607-1620, 1988
A;T-\$\frac{1}{2}\$ Levy. B.; Levy, S.
A;T-\$\frac{1}{2}\$ Levy. B.; Levy, S.
A;Reference number: JL0061; MUID:89035985; PMID:3141553
A;Accession: JL0062
A;Molecule type: mRNA
A;Residues: 1-120 <CCARA;Cross-references: EMEL:X14098
A;Cross-references: EMEL:X14098
A;Cross-references: EMEL:X14098
A;Cross-references: EMEL:X14098 Best Local Similarity
Matches 9; Conserv Query Match 102 QORSSYPFT 110 1 QORSSYPFT 9 Conservative 100.0%; Score 48; DB 2; Length 132; 100.0%; Pred. No. 0.023; 0; Mismatches 0; predicted <MAT> murine B cell lymphoma. An explana Indels 0 Gaps 0

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C;Superfamily: in
C;Keywords: heter
F;16-89/Domain: i
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A; Residues: 1-106 < AGA>
A; Residues: 1-106 < AGA>
A; Cross-references: GB: 568985; NID:g545746; PIDN:AAB30096.1; PID:g545747
A; Cross-references: GB: 568985; NID:g545746; PIDN:AAB30096.1; PID:g545747
A; Experimental source: spleen and myeloma cell line MOPC 315.43
A; Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
A; Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
RESULT
E38601
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J. Exp. Med. 170, 1-13, 1989
A;Title: Functional immunoglobulin light chain genes are
A;Reference number: A92781; MUID:89310348; PMID:2501443
A;Accession: PS0070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig light chain V region anti-triplex DNA - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B54378
R;Agazie, Y.M:; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
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                                                                                                                       á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V region (38C13.V6.1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
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A;Accession: B54378
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                        ;Molecule type: DNA
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                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin; 16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                     Matches
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Best Local
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Pred. No.
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Pred. No. 0.29;
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Pred. No. 0.26;
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R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A,Fitle: Common structural features among monoclonal antibodies binding the A;Reference number: A38601; MUID:91115823; PMID:1703527

A,Accession: E38601
                                                          C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;8-81/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                      R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G. Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
A;Accession: S17626
                                                                                                                                                                                                                                                                                                                Ig kappa chain V region - mouse C;Species: Mus musculus (house mouse) C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21eJan-2000 C;Accession: S17626
                                                                                                                                 A; Molecule type: nucleic acid
A; Residues: 1-91 < CLA>
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A; Residues: 1-99 < GOS>
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A;Title: Common structural features among monoclonal antibodies binding the A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: D38601
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A; Residues: 1-35 < GOS>
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C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991
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                       Query Match
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87.5%;
79.2%;
88.9%;
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  Score 38;
Pred. No.
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Pred. No. 0.7;
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Pred. No. 0.26;
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1.6;
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RESULT 8
S42466
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G27887
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F;38-111/Domain: immnoglobulin homology <INM>
F;46-55/Region: complementarity-determining 1
F;71-77/Region: complementarity-determining 2
F;110-118/Region: complementarity-determining 3
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0013
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A;Reference number: S42466
A;Accession: S42466
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42466
R;Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
  Ig kappa chain V region (H18-S415) -
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revisio
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-iditypic antibody that induces
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Structural basis of stimulatory anti-idiotypic antibodies. A;Reference number: PL0011; MUID:88142863; PMID:3125424 A;Accession: PL0013
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A;Residues: 1-140 <CHE>
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Best Local
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7; Conserva
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25, 33-40, 1988
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#sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
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88.9%;
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Pred. No.
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RESULT 12
S40334
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A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus k
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain precursor V region (MRL22) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Structural and functional implications of a restricted antibody response to A;Reference number: A91043; MUID:86300658; PMID:2427335 A;Accession: G27887
                                                                                                      C;Superfamily: immunoglobulin V region; imm
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-132 <KLE>
A;Cross-references: EMBL:X72444
                                                                                                                                                                                                                               R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi
A;Reference number: $40312; MUID:94080891; E
A;Accession: $40334
                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-130 < KOF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization
A;Reference number: A94689; MUID:88331394, PMID:3138286
A;Accession: A32513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A32513
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A;Residues: 1-106 <CAT>
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                                                                                     F;37-111/Domain: immunoglobulin homology <IMM>
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77.8%;
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Pred. No. 3.6;
0; Mismatches
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Pred. No. 3;
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                                         Length 132;
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A;Gene: FlyBase:rEbgn0002938
A;Crosa-references: FlyBase:FBgn0002938
C;Superfamily: ninaC protein; myosin motor domain homology; protein kinase homology
C;Keywords: actin binding; alternative splicing; ATP; nucleotide binding; P-loop; phosph
F;14-282/Domain: protein kinase homology <KIN>
F;335-1022/Domain: myosin motor domain homology <MMOT>
F;425-432/Region: nucleotide-binding motif A (P-loop)
F;911-936/Region: actin binding #status predicted
F;1054-1501/Domain: carboxyl-terminal <CBT>
F;445,60,145/Active site: Lys, Glu, Asp #status predicted
F;431/Binding site: ATP (Lys) #status predicted
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penicillin-binding proteins 1A/1B ponA [imported] -
C;Species: Bacillus halodurans
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-86 < SHE>
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. Biol. Chem. 263, 4059-4063, 1988

.Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid

.Reference number: A28195; MUID:88153717; PMID:3267217

.Recession: C28195
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Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-May-1997

Accession: C2819-
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;Residues: 1-1501 <MON>
;Cross-references: GB:M20230; NID:g157967; PIDN:AAA28721.1; PID:g157968
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Best Local
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2.7.1.-)
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Pred. No. 3.9;
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                                       Bacillus halodurans (strain C-125)
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Search completed: July 30, Job time: 3.66113 secs
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A;Residues: 1-866 <STO>
A;Cross-references: GB:AP001512; GB:BA0000004; NID:g10174030; PIDN:BAB05421.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: F83862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
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Best Local Similarity
Matches 6; Conser
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75.0%;
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1; Mismatches
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Result
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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KV1V_HUMAN
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Q20799
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Q57508
Q9x9k2
Q9mut3
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Q10442
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P04430
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P03713
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1 saccharomyc
7 schizophyll
3 bacillus su
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3 mesostigma
2 kluyveromyc
9 caenorhabdi
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13-AUG-1987
13-AUG-1987
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CONFLICT
SEQUENCE
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ACT_SITE
DOMAIN
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SMART; SM00242; MYSC; 1.

SMART; SM00220; S_TK; 1.

PROSITE; PS50096; TQ; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00109; PROTEIN KINASE TOM; 1.

PROSITE; PS0011; PROTEIN KINASE MON; 1.

Cytoskeleton; Actin-binding; ATP-binding; Myosin; Trans
Serine/threonine-protein Kinase; Alternative splicing.

DOMAIN

16
282
PROTEIN KINASE.
MEDLINE=86174817; PubMed=3083240; Dwulet F.E., O'Connor T.P., Benson "Polymorphism in a kappa I primary Mol. Immunól. 23:73-78(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00193; MYOSINHEAVY.
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InterPro; IPR001609; myosin head.
InterPro; IPR001719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                         Ig kappa chain V-I region Homo sapiens (Human).
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                                                SEQUENCE.
                                                                     NCBI_TaxID=9606;
                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                            Eukaryota;
                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
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GO:0004674; F:protein serine/three 

GO:0016062; P:adaptation of rhodop 

GO:0017010; P:cytoskeleton.organiz 

GO:00016039; P:deactivation of rhod 

GO:00016039; P:bhototransduction, v 

GO:0001604; P:protein localization
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Pred. No. 16;
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/FTId=VSP_004940.
Missing (In isoform Short).
/FTId=VSP_004941.
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K -> Q (IN REF. 1; AAA28720/AAA28721)

P -> R (IN REF. 1; AAA28721).
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AFRGFRDPVRLPPLVNEKSGQLNENTADFIRPFAKKWREKS
IFQVLLHYRAARF -> GKKTQVDRLREYDEEHIDISETPS
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ATP
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                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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           protein (BAN).";
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P01618;
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HSSP; P80362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                        PIR;
                                                                                                                                                                                                                                                                                                                                                                             canine myeloma immunoglobulin: evidence predated mammalian speciation."; predated mammalian speciation."; Immunochemistry 15:303-305(1978).
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21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
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             DISULFID
                                                                                                                                                                                                SMART;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                            -!- MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
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                                  DOMAIN
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### 15006; IS_v ### 15006; IS_v ### 15006; IS_v ### 150047; IS_v ### 15004
                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: THE SEQUENCE OF THE THIS MYELOMA PROTEIN HAS ALSO BEEN
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TE; PS50835; IG_LIKE; 1.
loglobulin V region; Amylo
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IPR003596; Ig_v.
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Pred.
                              FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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COMPLEMIARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUBUNCE TOY. N.1...

STRAIN=EI Tor N.1691 / Serotype 01;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Grmolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIBCH
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                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                        "The chemotactic response of Vibrio anguillarum to fish intestinal mucus is mediated by a combination of multiple mucus components.";

J. Bacteriol. 181:4308-4317(1999).

-i- FUNCTION: METHYLATION OF THE MEMBRANE-BOUND METHYL-ACCEPTING CHEMOTAXIS PROTEINS (MCP) TO FORM GAMMA-GLUTAMYL METHYL ESTER RESIDUES IN MCP (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + protein L-glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9KQ06; Q9KCL5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemotaxis protein methyltransferase CHER1 OR CHER OR VC2201.
                                                                                                             EMBL; AE004291; AAF95346.1; -. EMBL; AF139167; AAD45254.1; -. PIR; H82106; H82106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O'Toole R.,
                InterPro; IPR000780; Ch
InterPro; IPR001601; Me
Pfam; PF01739; CheR; 1.
Pfam; PF03705; CheR_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cholerae.
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STRAIN=El Tor N16961 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHR1_VIBCH
                                                                             HSSP; P07801; 1AF7.
TIGR; VC2201; -.
                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wolf-Watz H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99328977; PubMed=10400589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 10-266 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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                                                                                                                                                                                                                                                                                                         = S-adenosyl-L-homocysteine + protein L-glutamate methyl e SIMILARITY: Contains 1 cheR-type methyltransferase domain.
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   CHERMTFRASE
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12005 MW;
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75.0%;
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                                                                CheR_Metranf
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Pred. No.
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se 1 (EC 2.
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CYS1_DICDI
CYS1_DICDI
ID _CYS1_I
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DT 13-AUG
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GN CPRA C
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HEAD_LAMBD
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Best Local S
Matches 6
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Best Local Similarity
Matches 6; Conserv
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"Nucleotide sequence of bacteriophage lambda DNA.";
J. MOL. Biol. 162:729-773(1982).
-I- FUNCTION: GENE B PROTEIN IS A MAJOR COMPONENT OF THE PHAGE HEAD THERE ARE ABOUT 420 COPIES OF PROTEIN E DER MATURE PHAGE. SOME THE E PROTEIN IS COVALENTLY LINKED MITH AN EQUIMOLAR AMOUNT OF PROTEIN C AND CLEAVED TO YIELD MINOR CAPSID PROTEINS X1 AND X2.
-I- SIMILARITY: STRONG, TO MAJOR HEAD PROTEIN OF PHI-80 AND P21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEAD LAN
P03713;
                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Methyltransferase; Complete proteome.

DOMAIN

1 275
CHER-TYPE METHYLTRANSFERASE
SEQUENCE 275 AA; 30871 MW; F008ADCBFA46A921 CRC64;
                                                                                                                                                                                                                                                                                                  EMBL; J02459; AAA96540.1; -. PIR; H04333; VHBPEL.
                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinf the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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Coulson A.R., Hong G.F.,
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21-JUL-1986 (Rel.
01-JUN-1994 (Rel.
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Transferage. Manharm
                                                                                                                                                                                                                                                                        InterPro; IPR005564; Phage_cap_E. Pfam; PF03864; Phage_cap_E; 1.
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Lambda-like viruses.
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85.7%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                    Usage
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13-AUG-1987 (Rel. 05, 13-AUG-1987 (Rel. 05, 28-FEB-2003 (Rel. 41, Cysteine proteinase 1 CPRA OR CP1.

05, Created)
05, Last sequence update)
41, Last annotation update)
se 1 precursor (EC 3.4.22.-)

CYS1_DICDI P04988;

STANDARD;

PRT;

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Matches 6
                                                                                              DISÜLFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contains N-acetylglucosamine-1-phosphate bound to serine mannose-6-phosphate on N-linked oligosaccharides.";
J. Biol. Crysteine proteinases 1 and 2 are Believed in The Breakhoun OF PROTEIN URING DIFFERENTIATION C DICTYOSTEIUM AS A RESPONSE TO STARVATION.

-I. SUBCELIULAR LOCATION: Lysosomal.
-I. PTM: PHOSPHOGLYCOSYLATED, CONTAINS GLCNAC-ALPHA-1-P-
                                                                                                                                              CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                         ProDom; PD000158; Peptidase_C1; 1.

SMART; SM00645; Pept_C1; 1.

PROSITE; PS000139; THIOL_PROTEASE_CYS; PROSITE; PS00639; THIOL_PROTEASE_ASN; PROSITE; PS00640; THIOL_PROTEASE_ASN;
                                                                                                                                                                                                                                                                                                              GlycoSuiteDB; P04988; -.
SWISS-ZDPAGE; P04988; DICTY.
DictyDb; DD02003; CprA.
InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; SHprot_acBite.
Pfam; PF00112; Peptidase_C1; 1.
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PIR; A22827; KHDO.
HSSP; P25779; 1AIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-85257519; PubMed-2990918;
Williams J.G., North M.J., Mahbub
                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement
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Manzi A., Freeze H.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE OF CARBOHYDRATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                    Hydrolase; Thiol protease; Lysosome; Zymogen; Phosphorylation; Signal.
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209
                39)
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                                               Similarity 6; Conserv
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Best Local Similarity
Matches 6; Conserv
STRAIN=972;
STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne Sgouros J., Peat N., Hayles J., Baker S., Basham D., Sgouros K., Brown D., Brown S., Chillingworth T., Chu;
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Q10442;
01-OCT-1996
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SEQUENCE
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15-JUL-1999
                                                                                                                   Eukaryota; Fungi; Ascomy
Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE-79237924; PubMed=112021; Eulitz M., Kley H.-P., Zeitler H.-J.; Eulitz M., Kley H.-P., Zeitler H.-J.; "The primary structure of the Bence-Jones protein Kue. T sequence of the variable part of a human L-chain of the Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979). Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979). -I- MISCELLANEOUS: THE C. REGION OF THIS CHAIN HAS THE IN MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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P01604;
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28-FEB-2003
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                                                                        SEQUENCE FROM N.A.
                                                                                            NCBI_TaxID=4896
                                                                                                        Schizosaccharomyces.
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(Rel.
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Rel. 01, Last sequence. 38, Last annotation. V-I region Kue.
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88
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107
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Primates;
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scomycota; Schizosaccharomycetes;
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Pred. No.
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COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-4.
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COMPLEMENTARITY-DETERMINING-2.
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RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
Ames K., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Moodward J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Vonstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vonstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";

The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 7
                        P42251;
01-NOV-1995
01-NOV-1997
15-SEP-2003
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PIR; T37576; T37576
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                                                                                                PPBD_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
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Pfam; PF00153; mito_carr; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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              Alkaline
                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GeneDB_SPombe; SPAC12B10.09;
InterPro; IPR002067; Mit_car
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SIMILARITY: Belongs to the mitochondrial carrier family.
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            995 (Rel. 32, Created)
997 (Rel. 35, Last sequence update)
003 (Rel. 42, Last annotation update)
phosphatase D precursor (EC 3.1.3.1)
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RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot P., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Grims C., Fujita M., Fujita Y., Fuma S., Gallzri A., Galleron N.,
RA Ghims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Schiguchi J., Sekowaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Scookin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wandbutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT Subtilis.";
                                                                                                                                                                      "Purification and characterization of extracell membrane-bound insoluble alkaline phosphatases phosphodiesterase activities in Bacillus subtil J. Bacteriol. 134:100-107(1978).
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Microbiology 142:2041-2047(1996).
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STRAIN=168;
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NCBI_TaxID=1423;
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[4]
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                                    This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                       Yamane K.,
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=78171419; PubMed=25878;
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                                                                                              alcohol + phosphate.
-!- INDUCTION: By phosphate starvation.
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       the
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       Swiss Institute of
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Carter N.M.,
Daniel R.A.,
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30-MAY-2000 (I
28-FEB-2003 (I
                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                Submitted (DEC-1998) to the EMBL/GenBar-i- SIMILARITY: Contains 1 SET domain.-i- SIMILARITY: Contains 1 TTL domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; D69676; D69676.
SubtiList; BG11174; phoD.
InterPro; IPR001952; Alk phosphtse.
InterPro; IPR006311; Tat.
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PIR; [
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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                                           SEQUENCE
                                                                                                                                                                            EMBL; Z47808; CAA87778.1;
                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    modified and this statement
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between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                Mortimore B., Matthews
                                                                                                                                                                                                                                                                                                                        STRAIN-Bristol N2;
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TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
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                                                                                                  InterPro; IPR001214; SET.
InterPro; IPR004344; Tub_tyr_lygase.
                                                                                                                         WormPep; D2013.
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Z47809; CAA87783.1; -.
Z47808; CAA87783.1; JOINED.
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  Similarity 5; Conser
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                                           662
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(Rel.
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larity 55.6%;
Conservative
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39, Last sequence 41, Last annotation
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76750 MW;
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Last annotation updat
protein D2013.9 in ch
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Score 33; DB Pred. No. 43; 3; Mismatches
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Pred. No.
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TF2D_STRPU
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Matches
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                                                                                                       CN7B MOUSE
Q9QXQ1;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rybacki I., Childs G.;

Rybacki I., Childs G.;

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION

FUNCTION: GENERAL FACTOR TRANSCRIBED BY RNA POLYMERASE II. THILD BINDS
            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
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                                                                cAMP-specific
                                                                              16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U86586; AAB47272.1;
HSSP; P20226; 1TGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strongylocentrotus purpuratus (Purple sea urchin) Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription initiation factor TFIID (TATA-box
(TATA sequence-binding protein) (TBP).
                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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                                                   PDE7B.
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                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00352; TBP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Echinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                            interPro; IPR000814; TFIID.
                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Binds DNA as a monomer. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TF: SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES THE POSITION OF TRANSCRIPTION INITIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE TBP FAMILY.
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                                                               (Rel. 40, Created)
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(Rel. 41, Last annotation update)
ic 3',5'-cyclic phosphodiesterase
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                                                                                                                                                                                                                                                                                                                                                   regulation; DNA-binding; Nuclear protein;
                                                                                                                                    STANDARD;
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            Chordata;
Rodentia;
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85.7%;
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            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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RESULT 13
CN7B HUMAN
ID CN7B G
AC QNNP56
DT 16-OCT
DT 15-SEP
DE CAMPS6
GN PDE7B.
OS HOMO 8
OC MAMMAL
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WA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;

"Cloning and characterisation of the human and mouse PDE7B, a novel TAMP-specific nucleotide phosphodiesterase.";

RL Biochem. Biophys. Res. Commun. 272:186-192(2000).

C.: FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL C.: CATALYTIC ACTIVITY: Adenosine 1',5'-cyclic phosphate + H(2)O = C.: CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O = C.: COPACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).

C. I. COPACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).

C. I. ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.

C. I. ENZYME REGULATION: INTERNAM, AND MILITIONE.

C. I. ENZYME REGULATION: Highly expressed in brain.

C. I. TISSUE SPECIFICITY: Highly expressed in brain.

C. I. DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.

C. I. SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE

SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 5
                                                                                                          CN7B HUMAN
Q9NP56;
16-OCT-2001
16-OCT-2001
15-SEP-2003
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SEQUENCE FROM N.A.
MEDLINE=20087273; PubMed=10618442;
Hetman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
"Cloning and characterization of PDE7B, a cAMP-specific phosphodiesterase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF190639; AAF25195.1; -. EMBL; AJ251859; CAB92530.1; -. MGD; MGI:1352752; Pde7b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N. STRAIN=C57BL/6J;
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; cAMP. DOMAIN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00387; PDIESTERASE1.
SMART; SM00471; HDc; 1.
                                                    Homo sapiens (Human)
                                                                                        cAMP-specific
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InterPro; IPR002073; PDEase.
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5; Conserv
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                                                                                  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
ic 3',5'-cyclic phosphodiesterase
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51337 MW;
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Pred. No. 4
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RESULT
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        SCD5 YEAST
P34758;
01-FEB-1994
01-FEB-1994
                                                    YEAST
                                                                                                                                                                                                                                                              MIM; 604645; -. GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS. GO:00007165; P:signal transduction; TAS. GO:00007268; P:synaptic transmission; TAS. InterPro; IPR003607; Met_phsphohydro. InterPro; IPR002073; PDEase.
                                                                                                                                                                                                 PROSITE; PS00126; PDEASE I; 1.
Hydrolase; cAMP; 3D-structure.
DOMAIN 172 410 C.
                                                                                                                                                                                                                                                                                                                                                EMBL; AB038040; BAA96537.1;
EMBL; AJ251860; CAB92441.1;
PIR; JC7266; JC7266.
PDB; 1LXW; 26-JUN-02.
                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20329226; PubMed=10872825; Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.; "Cloning and characterisation of the human and mouse PDE7B, a novel
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sasaki T., Kotera J., Yuasa K., Omori K.;
"Identification of human PDE7B, a cAMP-specific phosphodiesterase.";
Biochem. Biophys. Res. Commun. 271:575-583(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      SMART;
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                                                                                                                                                                                                                                   ; PR00387; PDIESTERASE1.
SM00471; HDC; 1.
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HGNC:8792; PDE7B.
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                                           STANDARD;
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                                                                                                                                                       Score 32;
Pred. No.
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28-FEB-2003

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Query Match
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Submitted
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EMBL; U42227; AAA85443.1; -.
EMBL; Z49821; CAA89976.1; -.
EMBL; Z75237; CAA99650.1; -.
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Song J.M., Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: PUTATIVE TO FORM.... -- SUBCELLULAR LOCATION: Membrane-associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97051586; PubMed=8896263;
Parle-Mcdermott A.G., Hand N.J., Goulding S.G., Wolfe McGuence of 29 kb around the PDR10 locus on the right Saccharomyces cerevisiae chromosome XV: similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288c;
Wang W., Zhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nelson K.K., Holmer M., Lemmon S.K.; "SCD5, a suppressor of clathrin deficiency, encodes with a late secretory function in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a
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Submitted (NOV-1993) to
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SUBUNIT: PUTATIVE 10-FORMYL-TETRAHYDROFOLATE
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OR FTB1
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 Similarity 5; Conser
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OR YOR329C.
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er M., Lemmon S.
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97305
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55.6%;
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Score 32; DB Pred. No. 92; 2; Mismatches
                                                                Membrane; Repeat.
3 X 20 AA APPROXIMATE REPEATS
                                                    C60F5BE8808E1D31 CRC64;
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Pfam; Pruv...,
PRINTS; PRO0119; CATATPASE.
PRINTS; PR00942; CUATPASEI.

R TIGREAMS; TIGRO1511; ATPASE-IB1 Cu; 1.
R TIGREAMS; TIGRO1525; ATPASE-B-Type; 3.
R TIGREAMS; TIGRO1494; ATPASE P-Type; 3.
DR TIGREAMS; TIGRO0003; TIGRO0003; 6.
DR PROSITE; PS00154; ATPASE_E1_E2; 1.
PROSITE; PS01047; HMA 1; 5.

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Pfam; PF00122; Pfam; PF00403; Pfam; PF00702;

HMA; E1-E2 InterPro;
InterPro;

IPR006121; | IPR005834; |

; Cu_ATPase1.
; Cu_bind_dom.
; HeavyMe_transpt.
; Hydrolase.
; Metal_bind.
2_ATPase; 1.

InterPro;

IPR006191;

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RESULT 15
AT7A_CRIGR
ID AT7A_(
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InterPro;
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or send a
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Mammalia; Eutheria;
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15-SEP-2003
                                                                                                                                                                                                                                                            modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Camakaris J., Petris M.J., Bailey L., Shen P., Lockhart P., Glower T.W., Barcroft C., Patton J., Mercer J.F.; "Gene amplification of the Menkes (MNK; ATP7A) P-type ATPass CHO cells is associated with copper resistance and enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96154683; PubMed=8589689;
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TISSUE SPECIFICITY: PO
SIMILARITY: Belongs to
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Q04656; 1AW0.
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IPR001877;
IPR006122;
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ION: MAY FUNCTION IN THE EXPORT INTRACELLULAR ORGANILLE. IT MAY
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remorting ATPase )
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; Chordata; Craniata; Vertebrata; Euteleostomi;
; Rodentia; Sciurognathi; Muridae; Cricetinae;
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FOUNDS IN MOST TISSUES EXCEPT LIVER.
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annotation update)
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Search completed: July 30, 2003, 09:45:08 Job time: 3.40532 secs
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66.7%; Score 32; DB 1; Length 1476;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
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HMA 4.

HMA 5.

HMA 6.

PHOSPHORYLATION (PROBABLE).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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IG; Copper; Repeat.

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

POTENTIAL.
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HMA 2.
HMA 3.
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34; Search time 6.96678 Seconds (without alignments) 333.364 Million cell updates/sec

Title: Perfect score: Sequence: US-09-865-198-6 48 1 QQRSSYPFT 9

Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:

830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database : SPTREMBL_23:* sp_archea:*
sp_bacteria:*
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sp_mhc:* sp_mammal:* human:* _invertebrate:*

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sp_phage:* sp_plant:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	5	4	ω	N	1	Result No.
34	34	34	34	34	35	35	36	36	37	37	37	37	37	38	42	Score
70.8	70.8	70.8	70.8	70.8	72.9	72.9	75.0	75.0	77.1	77.1	77.1	77.1	77.1	79.2	87.5	Query
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Q43448	024324	Q9SWC7	Q8FEW0	8X9X8D	Q12744	OFIVED	Q9KC72	Q8EXK4	Q9VM23	Q8EZ70	Q8UUZ5	Q18582	Q9U410	QUIVDDO	Q8K1F2	IB
Q43448 glycine max	O24324 phaseolus v	Q9swc7 glycine max	Q8few0 escherichia	Q8x6y8 escherichia	. Q12744 saccharomyc	Q8vij0 mus musculu	Q9kç72 bacillus ha	Q8exk4 leptospira	Q9vm23 drosophila	Q8ez70 leptospira	Q8uuz5 brachydanio	Q18582 caenorhabdi	Q9u410 schistosoma	Q8vdd0 mus musculu	Q8k1f2 mus musculu	Description

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	Q8sxd8 drosophila		Q95sl8 drosophila		a	Q91817 xenopus lae	Q92tj0 rhizobium m	Q9siy8 arabidopsis	Q9xzc2 drosophila	Q961n4 drosophila	Q9v490 drosophila		a	Q9w6e5 gallus gall	N	Q8svy7 encephalito	Q8k1f3 mus musculu	Φ	Q8mt33 drosophila	മ	rt		-		096750 trypanosoma	Q9k6q6 bacillus ha		096635 trypanosoma

ALIGNMENTS

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1 QQRSYPFT 9	Query Match 87.5%; Score 42; DB 11; Length 112; Best Local Similarity 88.9%; Pred. No. 0.47; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	SEQUENCE 112 AA; 11953 MW; 4716B87FADB543ED CRC64;	112 112	NON TER 1 1 1	M00406; IG	SMART; SM00409; IG; 1.	0047; ig; 1.	InterPro; IPR003596; Ig_v.	IPR007110;	IPR003599;	EMBL; AF516283; AAM64201.1;	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.	ains.";	"Innate proteolytic antibodies: Failed D-VIPase response to the D-	7	SEQUENCE FROM N.A.	[1]		Rodentia; Sciurognathi; Muridae;		s (Mouse)	light chain variable	(TrEMBLrel. 23, Last annotation	(TrEMBLrel. 22,	01-OCT-2002 (TrEMBLrel. 22, Created)		Q8K1F2 PRELIMINARY; PRT; 112 AA.	ሆ 1 ም2

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RESULT 2
Q8VDD0

Q8VDD0

Q8VD

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Q9U410
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Best Local
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 134 134
                       Pfarks
SMART;
                                                                                                                            SEQUENCE FROM N.A.

Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L.,

Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L.,

"Amplification, cloning and sequence analysis of the

"Amplification gene of monoclonal anti-idiotypic ant

Schistosoma japonicum.";

Schistosoma japonicum.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databas

EMBL; AF207620; AAR19434.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
Monoclonal anti-idiotypic ar
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Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
Anti-MOG Z12 variable light
                                                                                                                                                                                                                                                                                                                                                        Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
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    PROSITE;
                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                              variable region (Fragment)
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      PS50835;
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GV; 1.
IG_LIKE;
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87.5%;
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    Last sequence update)
    Last annotation update)
    antibody NP30 immunoglobulin light chain

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Last annotation update)
chain (Fragment).
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Pred. No.
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Best L
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 30.8 kDa protein.
C42D8.1.
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Q18582;
Q1-NOV-1996
Q1-OCT-2001
                                                                              Q8UUZ5
Q8UUZ5;
01-MAR-2002
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
0rthodenticle-related homeobox 5.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Actinopterygii; Neopterygii; Teleostei; Ostarioph
Cyprinidae; Danio.
NCBI_TaxID=7955;
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                   Submitted (JUN-2001) to the ENEMBL; U56966; AAA98721.2; -. WormPep; C42DB.1; CE27844. Hypothetical protein. SEQUENCE 269 AA; 30847 MW;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                      Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                Science
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                               Waterston
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77.8%;
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EMBL/GenBank/DDBJ
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Pred. No. 4
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                               Vertebrata; Euteleostomi;
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                     Cypriniformes;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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RESULT
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RESULT
Q9VM23
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DT 01
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InterPro; IPR007104; Paired homeo.
Pfam; PF00046; homeobox; 1.
Pfam; PF03529; TF Otx; 1.
PRINTS; PR01255; OTXHOWEOBOX.
PRODOm; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                      Q9VM23;
01-MAY-2000
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00389; HAMEDBOX 1; 1.

PROSITE; PS0007; HOMEDBOX 2; 1.

PROSITE; PS50071; HOMEDBOX 2; 1.

PROSITE; PS50552; PAX; 1.

PROSITE; PS50552; PAX; 1.

HOMEODOX; DNA-binding; Nuclear protein.

PROSITE; PS0552; PAX; 31422 MW; 542FA0F69AE90DAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Complete
SEQUENCE
                                    CG5125
                                                                                                                                 Q9VM23
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=56601 / Ser
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                    NINAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Spirochaetes;
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Gamse J.T., Liang
Drosophila melanogaster
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                  OR CG5125
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J.O., Shen Y.-C.,
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(Fruit fly)
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Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxerdale J., Bayraktaroglu L., Beasley E.M.,
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RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Posler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyam C.,
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Wang S.,
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Yel, Yeh R.-F., Zaveri J.S., Zhan M., Zhu S., Zhu X., Smith H.O.,
The genome sequence of Drosophila melanogaster.";
RI Science 287:2185.2195 (2000)
                                                                                                                                                                                                                                                                                                                                                                               Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., An Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., A Banzon J., Beeson K.Y., Busam D.A., A Carlson J.W., Center A., Champe M., Davemport L.B., Dietz S.M., A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., A Ferriera S., Frise E., Galle R.F., Gary N.S., George R.A., A Ferriera S., Prise E., Galle R.F., Gary N.S., George R.A., A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., A Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., A Phouanenavong S., Pittman G.S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Stapleton M., Strong R., Swirskas R., Tector C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Celniker S.E., Adams
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"Annotation of Drosophila melanogaster genome.";
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Ephydroidea; Drosophilidae; Drosophila.
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Pfam; PF00069; pkinase; 1.
ProDom; PD000355; myosin head; 1.
ProDom; PD0000355; myosin head; 1.
ProDom; PD000031; Prot kinase; 1.
SMART; SM00215; IQ; 2.
SMART; SM002242; MYSC; 1.
SMART; SM002249; MYSC; 1.
SMART; SM002219; TyrKC; 1.
SMART; SM002219; TyrKC; 1.
PROSITE; PS50096; IQ; 2.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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Bacteria; Spirochaetes;
NCBI_TaxID=173;
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01-MAR-2003 (TrEMBLrel.
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Mannosyltransferase A.
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InterPro;
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Adams M.D
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STRAIN=56601 / S
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Celniker (
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IPR001609; myosin head.
IPR000719; Prot kinase.
IPR002290; Ser_thr_pkinase.
IPR001245; Tyr_pkinase.
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Conservative
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                                                                                                                                                                                                                                                                                                   Icterohaemorrhagiae / Serovar lai;
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EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ
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Last annotation update)
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; Pred. No
                                                                                                                                         Score 36; DB
Pred. No. 29;
2; Mismatches
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Best Local S
Matches 6
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InterPro; IPR001264; Glyco_trans_51.
InterPro; IPR001460; Transpeptdse.
Pfam; PF00041; fn3; 1.
Pfam; PF00912; Transpeptdase; 1.
Pfam; PF0091895; Glyco_trans_51; 1.
ProDom; PD001895; Glyco_trans_51; 1.
                                                                                                             Eur. J. Immunol. 26:2225-2233(1996).
EMBL; U5915; AAB02917.1; -.
InterPro; IPR007110; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG L.

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SEQUENCE 108 AA; 118
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Q8VIJ0;
01-MAR-2002
01-MAR-2002
01-MAR-2003
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SMART; SM00060; FN3; 1
Hydrolase; Complete pu
SEQUENCE 886 AA; 98
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Q9KC72;
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Fuji F., Hirama C., Nakamura Y., O
Horikoshi K.;
                                                                                                                                                                                                                                                                                                           Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilken "Differences in V kappa gene utilization and VH CDR3 sequence anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C3H/HeJ-lpr/lpr;
MEDLINE=96409289; PubMed=8814271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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STRAIN=C-125 / JCM
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Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penicillin-binding proteins PONA OR BH1702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-DNA light
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(TrEMBLrel. 23, Last annotation update)
ght chain (Fragment).
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
pinding proteins 1A/1B.
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                                                                                      LIKE;
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     11859
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75.0%;
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     ₩;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Sciurognathi; Muridae;
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     68506D75613DBFBE CRC64;
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Ogasawara N.,
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., Kuhara S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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Q12744
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85284950; PubMed=3896774;
Weiss W.A., Friedberg E.C.;
"Molecular cloning and characterization of the expression of RAD10 protein in E. coli.";
EMBO J. 4:1575-1582(1985).
EMBL; Z46660; CAA86643.1; -.
EMBL; X02591; CAA26432.1; -.
SGD; S0004561; YML094C-A.
InterPro; IPR002016; Peroxidase.
                                                                                               21888 OR ECS2174 OR ECS1635.
Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                          01-MAR 2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation updat
Putative capsid protein of prophage CP-933X (Puta
SEQUENCE FROM N.A. STRAIN=0157:H7 / F MEDLINE=21074935;
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                                                                                                                                                                                                                                                                                                      Q8X6Y8;
                                                                                                                                                                                                                                                                                                                            Q8X6Y8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrell B., Rajandream M.A.;
Submitted (NOV-1994) to the
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-NOV-1996 (TrEMBLrel 01, La
01-MAR-2003 (TrEMBLrel 23, La
Hypochetical ORF IDENTICAL to
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                                                                                  NCBI_TaxID=83334;
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3 133 AA;
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                      EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEROXIDASE 1; 1:
; 15007 MW; B93
  EDL933 / ATCC 700
PubMed=11206551;
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STRAIN-06:H1 / CFF073 / PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Re
Rasko D., Buckles E.L., Liou S.-R., Boutin.
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.
Mobley H.L.T., Donnenberg M.S., Blattner F.
"Extensive mosaic structure revealed by the
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-1702
EMBL; AB016765; AAN81620.1; -.
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Q8FEW0;
01-MAR-2003
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SEQUENCE
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EMBL; AP002557; BAB35597.1; -.
EMBL; AP002555; BAB35597.1; -.
InterPro; IPR005564; Phage_cap_E.
Pfam; PF03864; Phage_cap_E; 1.
Complete proteome.
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MEDLINB=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7." Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
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341 AA; 38123 MW;
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Pred. No. 67;
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(C STRAIN=CV. Shi-Shi,
(C) CONW T.Y., Liu S.M., Lin T.Y., Hsing Y.I.C.;
(C) CHOW T.Y., Liu S.M., Lin T.Y., Hsing Y.I.C.;
(C) CHOW T.Y., Liu S.M., Lin T.Y., Hsing Y.I.C.;
(T) "Characterization of soybean seed maturation protein, PM33.";
(II Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

SEMBL; AF167986; AAD46920.1; -.

REMBL; AF167986; AAD46920.1; -.

REMBL; AF167986; PEPTIDASE_C1.

InterPro; IPR000168; Peptidase_C1.

InterPro; IPR000168; Peptidase_C1.

InterPro; IPR000169; SHprot acsite.

RP FAUNTS; PP00112; PEPTIDASE_C1; 1.

RP PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.

RP PROSITE; PS00639; THIOL_PROTEASE_ASN; 1.

RP PROSITE; PS00639; THIOL_PROTEASE_ASN; 1.

RP PROSITE; PS00639; THIOL_PROTEASE_HS; 1.
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InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; SHprot acsite.
Pfam; PP00112; Peptidase_C1; 1.
Propom; PD000118; Peptidase_C1; 1.
SMART; SM00645; Pept_C1; 1.
PROSITE; PS00640; THIOL_PROTEASE ASN; 1.
PROSITE; PS00640; THIOL_PROTEASE CYS; 1.
PROSITE; PS00640; THIOL_PROTEASE CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Moldavian; TISSUE=Cotyledon;
Senyuk V., Becker C., Muentz K.;
Senyuk V., Becker C., Muentz K.;
"Isolation of cDNA clone encoding cysteine proteinase (CP4) from a
cotyledon-specific cDNA library of germinating kidney bean seeds.";
Submitted (CCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 299955, CABL7077.1; -.
EMBL; 299955, CABL7077.1; -.
HSSP; P25779; IAIM.
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Phasecolus vulgaris (Kidney bean) (French bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Phaseolus.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
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377 /
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236
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377
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                                   Score 34; DB
Pred. No. 75;
                                                         CYSTEINE PROTEINASE.; 6576DEF3F1B26DA9 CRC64;
                                                                       POTENTIAL.
                             Mismatches
                                          DB 10; Length 377;
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Search completed: July 30, Job time: 9.07789 secs 2003, 09:42:44

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Minimum
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Maximum Match 100%
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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Match
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Gapop 10.0 , Gapext 0.5
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48
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                                                                                                                                                                                                       Length
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                          AAY97234
AAE13142
AAB82708
AAG63993
AAE25954
AAU74411
ABJ26723
AAE13144
      AAU74418
                                                                                                                                                                                                                                                                   SUMMARIES
Complementary dete
Humanised antibody
VEGF antagonist an
Complementarity de
Mouse anti-KDR p1C
Light chain comple
VEGF binding relat
Humanised antibody
Antigen-binding pr
                                                                                                                                                                                                     Description
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	AAW73184	19	130	93.8	45
	AAW73183	19	130	ω	45
	AAW73182	19	130	ω	45
	AAW73181	19	130	ω.	45
	AAW73180	19	130	Ü	45
Fragment of gangli	AAW73179	19	130	ω.	45
	835	20	129	ω	45
3	AAY28385	20	129	w	45
KM-796 and KM-750	332	15	129	'n	45
Ganglioside GM2 an	316	22	107	ω.	45
gang	315	22	107	93.8	45
BoNT/A Hc binding	691	24	52	Ψ	45
≫	691	24	52	'n	45
e gang	316	22	9	Ψ	45
ide fragme	839	20	9	Ψ	45
	317	19	9	'n	4 5
SNV-env leader/hum	084	22	330	00.	48
VEGF binding relat	ABJ26731	24	240	80.	48
	441	23	240	100.0	48
KDR binding immuno	596	23	240	80.	48
VEGF binding relat	673	24	238	00.	48
en-bind	442	23	238	00.	48
KDR binding immuno	96	23	238	8	48
н-		23	238	8	48
Streptocoo	72	23	131	00.	48
Mouse anti-KDR p1C	AAE25966	23	125	0	48
Cli vector	AAE28917	23	125	8	48
agonist a	7	22	125	8	48
1 11	314	22	125	8	48
inding rela	672	24	108	8	48
gen-binding	441	23	108	8	48
nti-KDR pi	595	23	108	00	48
gonist	271	22	108	8	
ble li	972	21	108	8	48
o acid sequen	G639	22	107	0	48
VEGF binding relat	ABJ26730	24	106	100.0	48

ALIGNMENTS

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RESULT 1
AAY97234
glioblastoma multiforme; hemangioblastoma; AIDS; central nervous system neoplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human.
                                     29-JAN-1999;
29-JAN-1999;
                                                                                                      03-AUG-2000.
                                                                                                                                                         Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                       Immunoglobulin; antibody; complementary determing region; CDR; VEGF; vascular endothelial growth factor; KDR; kinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody;
                                                                                                                                                                                                                                                                                                     Complementary determining region (CDRL3) of anti-SI(KDR) antibody.
                                                                                                                                                                                                                                                                                                                                    19-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                AAY97234;
                                                                                                                                                                                                                                                                                                                                                                                          AAY97234 standard; Protein; 9
            (IMCL-) IMCLONE SYSTEMS INC
                                                                            28-JAN-2000; 2000WO-US02180.
                                                                                                                                WO200044777-A1
                                     99US-0117726.
99US-0240736.
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Witte L;

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RESULT 2
AAE13142
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Best Local S
Matches 9
Inhibiting, growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with
                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540770
                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US10504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gs snw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vascular endothelial growth factor receptor; VBGPR; antagonist; tumour; cytostatic; light chain hypervariable region; VI; myelocytic leukaemia; lymphocytic; exythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               extracellular domain of the KDR receptor with the same affinity VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VBGF). The antibodies neutralise CDR activation. The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a triabody, a humanised antibody or a chimerised antibody. The immunoglobulin molecules bind specifically to an
                                                                                                                                                                                                                                                                                                                                                                                                                   WO200174296-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE13142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised antibody murine light chain hypervariable region (VL)
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                                                                                                                                                                                                (CORR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  applications in treating these conditions. This sequence encodes preferred heavy chain complementary determining region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mmunoglobulins of the invention.
                                                                        2001-662942/76.
DB; AAD21668.
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CORNELL RES FOUND I
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                                                                                                                                                                                              FOUND INC
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В S

Disclosure; Page 37; 42pp; English

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RESULT 3
AAB82708
BY A LEX A CAN A WAX WAX WAX B C X LEX B C X L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse region of the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody murine light chain hypervariable region (VL) CDR-3 used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                         (SUNN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenia antitumour; neoplasm; collagen-vascular disease; autoimmune die
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The methoderowth factor receptor (VEGFR) in mammals particularly humans.
                                                 chemotherapeutic
                                                                           administering
                                                                                                           Treating or controlling an angiogenic dependent condition (encoplasm, collagen-vascular or autoimmune disease) in mammal
                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2000;
31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            colon carcinoma; ovarian carcinoma; neuroblastoma;
glioblastoma multiforme; melanoma; therapy; light
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEGF antagonist
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9; Conserv
                                                                                                                                                                                                                                                                                                            IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                         SUNNYBROOK HEALTH SCI
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2000US-0539692
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                                                                              a combination
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Pred. No. 9.3e+05;
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                                                                              antiangiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  light chain; CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                 molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9;
                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease;
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of complementarity determining region 3 of the light chain variable region (see also AAB82702) of IMC-IC11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, to repether with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a mani-angiogenic molecule and a chemotherapeutic agent, to produce a
                                             Novel monoclonal antibody specific for human sialoadhesin diagnosis, prevention, treatment of allergy, asthma, eczem such as lymphoma, leukemia or systemic mastocytosis, in a
                                                                                                                                                                                                                                                                                    (SMIK )
  Claim 10;
                                                                                                                                                           WPI; 2001-570749/64
                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2000; 2000US-0187595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis; leukemia; eosinophil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity determining region of light chain of antibody 2C4
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                                                                                                                                                                                                                                    Abrahamson JA,
                                                                                                                                                                                                                                                                                    ) SMITHKLINE
) SMITHKLINE
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Page 34; 35pp;
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                                                                                                                                                                                                                                    Bochner B,
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BEECHAM PLC.
                                                                                                                                                                                                                                                                                       HOPKINS
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English
                                                                                                                                                                                                                                 Erickson-Miller CL,
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Pred. No.
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ches 0;
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                                                                           diseases
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AAG63991-93 represent the complementarity determining regions (CDRs)

Query Match

100.0%;

Score

48;

DB 23;

Length

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AAE25P

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                                                  The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FIK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VBGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR plC11 scFv antibody light chain complementarity determining region 3 (CDRL3) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                    Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR; foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor; VEGF; tumour growth; light chain complementarity determining region 3;
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Sequence
                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 11; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2001; 2001US-0976787.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD42819.
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(WITT/) WITTE L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA;
   ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide; 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p1C11; scFv antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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Pred. No.
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. 9.3e+05;
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RESULT 6
AAU74411
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                                                                                CC site located to the N terminus of the CH1 domain. (1) is useful for:

CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;

CC (vEGF) receptor; reducing tumour growth; inhibiting angiogenesis;

CC reducing endothelial cell proliferation; inhibiting VEGF induced

CC migration of human leukaemia cells; blocking interaction of a protein and

CC its ligand, promoting interactions between immune cells and target cells;

CC and in vivo and in vitro for investigative, diagnostic or treatment

CC enthods. The design of (1) provides for efficient production so that

CC substantially all of the antigen-binding proteins produced are assembled

CC in the desired configuration. (1) is bivalent and bispecific, homogeneous

CC and in tetrameric form. The heavy chain constant domains which constitute

CC the PC region (e.g., CH2 and CH3 for an IGG molecule) of a natural

CC antibody and which provide other antibody functions can be present. There

CC is no requirement for processing in vitro to obtain the complete product.

CC This peptide sequence represents the light chain variable domain

CC complementarity determining region L3 (CDRL3) incorporated into an

CC antigew-binding protein described in the method of the invention.
Query Match & Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 9; Conserv
                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhu Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-2000; 2000US-206749P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity determining region; CDR; CDRL3; antigen; cytostatic; angiogenesis inhibitor; vascular endothelial growth factor receptor; VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor; antibody light chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-2001; 2001WO-US16924
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                                                                                                                                                                                                                                                                                                                                                                                                        ntigen-binding site located to the N terminus of immunoglobulin (Ig) ight chain constant domain (CL domain), and P2 has an antigen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-106189/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 57;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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Score
Pred.
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; Mismatches 0;
No.
DB 23;
9.3e+05;
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                 Length 9;
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RESULT 8
AAE13144
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AC AAE:
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ABJ26723
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Best Local :
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                                                                                                                                                                                                                                           The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (WEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells callular finction of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse peptide relating to the invention.
              AAE13144;
                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         New bispecific antibodies having antigen-binding sites specific for first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia
                                        AAE13144 standard; Protein; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 49; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABT23301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bispecific antigen-binding protein; mouse; murine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-201468/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhu Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eukaemia cell;
                                                                                                                                                                                                                                                                                                                                                                                                                           or for treating tumors
                                                                                                                                                                Similarity
9; Conserv
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                                                                                                                                  QQRSSYPFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; antigen binding site; VEGF reeell; vascular endothelial growth factor;
                                                                                                                                                                Conservative
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                                                                                                                                                                            100.0%;
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                                                                                                                                                                           Score 48; DB 24;
Pred. No. 9.3e+05;
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                                                                                                                                                                  Mismatches
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                                                                                                                                                                                         Length 9;
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RESULT 9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                          involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody light chain fragment used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-662942/76.
N-PSDB; AAD21670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Homo sapiens
Chimeric - Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 16; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US10504.
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Antigen-binding protein; antibody light chain variable domain; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibod vascular endothelial growth factor receptor; VEGF;
                                                                Antigen-binding protein light chain variable domain (VH) #2.
                                                                                                                                   AAU74418;
                                                                                                                                                              AAU74418 standard; peptide; 106
                                                                                                                                                                                                                                                                                                                                                                             Sequence
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                 106
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larity 100.0%;
Conservative . 0
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Pred. No. 0.086;
Mismatches
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KW Cytc
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                                                                                                                                                                                                                           RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the FC region (e.g., CH2 and CH3 for an Ig molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a light chain variable domain (VH) incorporated into FV, an engineered protein containing a heavy chain variable domain and a light chain variable domain in one polypeptide chain, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are stably associated in an immunoglobulin like complex. PI has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CI domain), and P2 has an antigen-binding site located to the N terminus of the CHI domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor, reducing tumour growth; inhibiting anglogenesis; reducing endothelial cell proliferation; inhibiting VEGF induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2000; 2000US-206749P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell proliferation inhibitor.
                                                                      VEGF binding related protein SEQ ID No
                                                                                                               01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 61; Page 61; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-106189/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAY-2001; 2001WO-US16924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200190192-A2
                                                                                                                                                                                        ABJ26730 standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                                                                                                                                                          Similarity
9; Conserv
                                                                                                                                                                                                                                                                                    QORSSYPFT
                                                                                                                                                                                                                                                                                                                       QQRSSYPFT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                       106 AA;
                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 48; Dilarity 100.0%; Pred. No. 0.0 Conservative 0; Mismatches
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                    96
                                                                            23.
                                                                                                                                                                                                                                                                                                                                                                            0.086;
                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                              Length 106;
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                                                                                                                                                                                                                                                                                                                                                              Gaps
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leukaemia cell; vascular er bispecific antigen-binding

c; antibody; antigen binding site; VEGF receptor; mitogenesis; cell; vascular endothelial growth factor; tumour; cantigen-binding protein; mouse; murine.

0

Cytostatic;

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RESULT 11
AAG63987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
                                       07-MAR-2000; 2000US-0187595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus
                                                                 05-MAR-2001; 2001WO-US07193
                                                                                                                      WO200166126-A1
                                                                                                                                                ds snw
                                                                                                                                                                       allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis; leukemia; eosinophil.
                                                                                                                                                                                                   Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
                                                                                                                                                                                                                           Amino acid sequence of light chain variable region of antibody 2C4
                                                                                                                                                                                                                                                       26-NOV-2001. (first entry)
                                                                                                                                                                                                                                                                                                           AAG63987 standard; Protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 54; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New bispecific antibodies having antigen-binding sites specific for first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhu Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-2001; 2001US-301299P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-2002; 2002WO-US20332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003002144-A1
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)B; ABT23308.
                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                         1 QQRSSYPFT
SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                               QORSSYPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                               96
                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              0.086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 12
AAY97236
ID AAY977XX
AC AAY97
XX 109-DE
XX Inmun
KW VEGFF;
KW Kinas
KW Ogliob
KW centr
XX 309-NH
NO 03-AU
XX 29-JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                              WPI; 2000-505966/45.
N-PSDB; AAA53768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the light chain variable region of murine monoclonal antibody 204. This antibody binds to human sialoadhgain factor-2 (SAF-2). The antibody is useful for treating or preventing allergic rhinitis, allergies, asthma, anemia, eczema or diseases such as lymphoma, leukemia or systemic mastocytosis in a mammal. It is also useful for detecting the presence of a cell, especially eosinoghil in a sample, by detecting binding of the antibody to SAF-2. The antibody can be coupled to toxins, antiproliferative drugs or radionuclides to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGF; vascular endothelial growth factor; KDR; kinase insert domain containing receptor; multivalent; monovalent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variable light chain fragment of anti-SI(KDR) antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY97236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel monoclonal antibody specific for human sialoadhesin factor-2 for diagnosis, prevention, treatment of allergy, asthma, eczema or diseases such as lymphoma, leukemia or systemic mastocytosis, in a mammay -
                                                                                                                          Zhu Z,
                                                                                                                                                                                                                             29-JAN-1999;
29-JAN-1999;
                                                                                                                                                                                                                                                                                                     28-JAN-2000; 2000WO-US02180
                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                        WO200044777-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glioblastoma multiforme; hemangioblastoma; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      humanised antibody; chimeric antibody; tumour; diabody; triabody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY97236 standard; Protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Fig 2; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abrahamson JA,
Schleimer R;
                                                                                                                                                                           (IMCL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [mmunoglobulin; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells in areas of excessive SAF-2 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-570749/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QQRSSYPFT 9
                                                                                                                                                                         IMCLONE SYSTEMS INC
                                                                                                                            Witte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQRSSYPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                          99US-0117726.
99US-0240736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system neoplasms; AIDS associated Karposi's sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bochner B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complementary determing region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIDS; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                멂
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kikly KK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Novel immunoglobulin molecules binding kinase insert domain-containing

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ARESULT 13
ARAB2710
ID AABB2710
ID AABB2710
AC AABB2
AC AABB2
AC AABB2
AC VEGF
XX COLOR
CW ANTIL
CHIMC
OS Chime
OS Chime
OS Chime
FT Regic
FT Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  뭐
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chain antibody, a monovalent single chain antibody, a diabody, a triabody, a humanised antibody or a chimerised antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, because of the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hemangioblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the immunoglobulins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colon carcinoma; ovarian carcinoma; neuroblastoma;
glioblastoma multiforme; melanoma; therapy; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
vascular endothelial growth factor; angiogenesis; antiangiogenic;
antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor with the same affinity as vascular endothelial growth factor, used to, reduce tumour growth
                                                                               28-JAN-2000;
31-MAR-2000;
                                                                                                                                                                                                 29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                WO200154723-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF antagonist antibody IMC-1C11 light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB82710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB82710 standard; Protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 51; 55pp; English
    (SUNN-) SUNNYBROOK HEALTH SCI CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast carcinoma; lung carcinoma; prostate carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQRSSYPFT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQRSSYPFT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus
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                                                                           2000US-0178791.
2000US-0539692.
                                                                                                                                                                                                     2001WO-US02839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "complementarity determining region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= CDR-L3
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100.0%; Pred. No. 0.088;
                                                                                                                                                                                                                                                                                                                                                                                                                                            "complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an capiogenic dependent condition in a mammal, especially a human.

The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent.

The anti-angiogenic molecule inhibits or blocks the action of a regression or arrest of the conditions that can be treated include and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; immunoglobulin; kinase insert domain-containing receptor; KD foetal liver kinase; FLK-1 receptor; vascular endothelial growth fa VEGF; tumour growth; light chain variable region; VL; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse anti-KDR p1Cl1 scFv antibody VL region
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100.0%; Pred. No. 0.088;
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RESULT 15
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N-PSDB;
The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an
                                                                                                                              New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR plCl1 scFv antibody
                                                                                        Claim 57; Page 57; 64pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen-binding protein; antibody light chain variable domain; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF;
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Pred. No. 0.088;
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                                                                                                                                                                                                                                                                 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor:
CC (VEGF) receptor, reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting angiogenesis;
CC endigration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient produced are assembled
CC in the design of (I) provides for efficient produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC entibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product:
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain (NH) incorporated
CC into for the invention of the inventio
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Matches
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QQRSSYPFT 96
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Search completed: July 30, 2003, 09:36:47 Job time : 9 secs

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Result
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Listing first 45 summaries
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Perfect score:
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1: //cgn2 6/ptodata/1/pubpaa/USO7
2: //cgn2 6/ptodata/1/pubpaa/PCT N
3: //cgn2_6/ptodata/1/pubpaa/USO6_
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/ Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US08_REW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09_RUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09_RUBCOMB.pep:*
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                      10 US-09-865-198-6

11 US-09-798-689-6

12 US-10-232-187-10

US-09-976-787-24

10 US-09-865-198-23

11 US-09-865-198-8

12 US-09-798-689-8

13 US-09-865-198-8

14 US-09-865-198-8

15 US-09-865-198-8

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Sequence 6, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 24, Appl
Sequence 23, Appl
Sequence 8, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 8, Appli
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Sequence 6, Appli
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Sequence 29, Appl
Sequence 29, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
                                                                                                                                                                                                                                                                                                                                                        Description
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APPLICANT: Witte, Larry
ITITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOPTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 6
LENGTH: 9
TYPE: DET
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ALIGNMENTS

RESULT 1 US-09-976-787-6

GENERAL INFORMATION:

Sequence 6, Application US/09976787 Patent No. US20020064528A1

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US-09-865-198-6; Sequence 6, Application US/09865198; Patent No. US20020103345A1; GENERAL INFORMATION:
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Best Local S
Matches 9
APPLICANT: Zhu, Zhenping
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9; Conserv
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                                                    Sequence 10, Application US/10232187 Publication No. US20030092091A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Goldstein, Neil I.

APPLICANT: Goldstein, Neil I.

TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689

CURRENT FILING DATE: 2001-03-02

CURRENT FILING DATE: 2001-03-02
                  APPLICANT: Abrahamson, Julie A. APPLICANT Bochner, Bruce
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CURRENT FILING DATE: 2001-05-24
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ORGANISM: Mouse
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FILING DATE: 1996-09-03
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Erickson-Miller, Connie L.
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                                      US-09-865-198-23; Sequence 23, A)
                                                                                   RESULT 6
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APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KD
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR PILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
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L'ENGTH: 106
TYPE: PRT
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CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/187,595
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: PCT/US01/07193
PRIOR FILING DATE: 2001-03-05
PRIOR PLICATION NUMBER: 60/315,943
PRIOR APPLICATION NUMBER: 60/349,830
PRIOR APPLICATION NUMBER: 60/349,830
Patent No. US20020103345A1 GENERAL INFORMATION:
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Matches 9; Conserv
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Patent No. US20020064528A]
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 8.0 for Windows
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TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies
FILE REFERENCE: GH50042-1
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                                          Application US/09865198
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100.0%; Pred. No. 0.09;
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Pred. No. 4e+05;
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APPLICANT: Zhu, Zhenping TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho

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; ORGANISM: Mouse
US-09-798-689-8
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LENGTH: 10
                                                                          GENERAL INFORMATION:
                                                                                        Sequence 4, Application US/10232187 Publication No. US20030092091A1
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ORGANISM: Mouse
-09-865-198-23
                                                                                                                                                                                                                                                                                   Query Match
Best Local (
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-1
PRIOR APPLICATION NUMBER:
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APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
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FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
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PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
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PRIOR APPLICATION NUMBER: 09/401,163
                                      APPLICANT: Abrahamson, Julie A. APPLICANT: Bochner, Bruce
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APPLICATION NUMBER: 08/326,552
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Bochner, Bruce
Erickson-Miller, Connie L.
Kikly, Kristine K.
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100.0%; Pred. No. 0.09;
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                                                                                                               US-09-865-198-8
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CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/1187,595
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: PCT/US01/07193
PRIOR APPLICATION NUMBER: 60/315,943
PRIOR APPLICATION NUMBER: 60/315,943
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
                                                   Sequence 8, Application US/09865198
Patent No. US20020103345A1
GENERAL INFORMATION:
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Best Local
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NUMBER OF SEQ ID NOS:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor
TITLE OF INVENTION: Production
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect 8.0 for Windows
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TYPE: PRT
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ITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies
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Pred. No. 0.092;
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Pred. No.
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APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
FITTLE OF INVENTION: Antibodies Specific to KDI
FILE REFERENCE: 11245/45505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-01-28
PRIOR PILING DATE: 1999-01-29
NUMBER OF*SEQ ID NOS: 40
PRIOR FILING DATE: 1999-01-29
NUMBER OF*SEQ ID NOS: 40
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US-09-881-823-6
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Patent No. US20020064528A1
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Best Local &
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LENGTH: 108
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries FILE REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
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PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
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CURRENT FILING DATE: 2001-05-24
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ORGANISM: Murine
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ORGANISM: Mouse
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US20020068066A1
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WIMS, LETITIA
CHEN, LI
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Pred. No. 0.11;
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Pred. No. 0.092;
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; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29
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US-09-798-689-21
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US-09-865-198-28
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Thes 9; Conserve
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LENGTH: 238
TYPE: PRT
                                              PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1996-09
PRIOR PELICATION NUMBER:
PRIOR FILING DATE: 1995-06
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1994-10
PRIOR PILING DATE: 1994-02
PRIOR FILING DATE: 1994-02
SOFTWARE:
SEQ ID NO 21
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Matches 9; Conserv
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                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                           PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1997-11-10
                                                                                                                                                                                                                                              APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Method for Reducing Tumc
TITLE OF INVENTION: Combined with Radiation
FILE REFERENCE: Sequence Listings 1-41 for
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/401,163
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CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
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TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
TITLE OF INVENTION: Production
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Pred. No. 0.2;
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Sequence 28, Application US/09976787

Patent No. US20020064528A1

GENERAL INFORMATION:

APPLICANT: Witte, Larry

ITITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245/46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 09/493,539

PRIOR PFILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 28

LENGTH: 240

TYPE: PRT

ORGANISM: Mouse

US-09-976-787-28
Search completed: July 30, 2003, 10:20:29 Job time: 11.0631 secs
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US-09-798-689-21
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US-09-976-787-28
                                                                                                                                                                             Query Match 100.0%; Score 48; DB 9; Length 240; Best Local Similarity 100.0%; Pred. No. 0.2; Matches 9; Conservative 0; Mismatches 0; Indels
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220 QQRSSYPFT 228
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Matches

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Query Match 93.8%; Score 45; DB 2; Leng Best Local Similarity 88.9%; Pred. No. 2.5e+05;	US-08-116-778E-11 Sequence 11, Application US/08116778E Patent No. 5830470 GENERAL INFORMATION: APPLICANT: KOIKE, MASAMICHI APPLICANT: KOIKE, MASAMICHI APPLICANT: HANAI, NOBUO APPLICANT: HASEGAWA, KENYA APPLICANT: HASEGAWA, MAMORU TITLE OF INVENTION: HUMANIZED ANTIBODIES NUMBER OF SEQUENCES: 49 CORRESPONDENCE ADDRESS: ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA COUNTRY: U.S.A. ZIP: 2201-4714 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/116,778E FILING DATE: 07-SEP-93 CLASSIFICATION NUMBER: US/08/116,778E FILING DATE: 07-SEP-9 TREJECOMMUNICATION INFORMATION: INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LEEGTH: 9 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: pobtide	ALIGNMENTS	28
Length 9;			Sequence 44, Appl Sequence 51, Appl Sequence 32, Appl Sequence 34, Appl Sequence 12, Appl Sequence 102, Appl Sequence 102, Appl Sequence 93, Appl Sequence 94, Appl Sequence 97, Appl Sequence 97, Appl Sequence 97, Appl Sequence 98, Appl Sequence 99, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl

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Best Local Similarity
Matches 8; Conserva
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APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
THE CONTINUES. (7071816.4000)
                                                                                                                                 GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                  APPLICANT:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                  TITLE OF
                                                 PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
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                                                                                                                                                  9, Application US/08483528B
5939532
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                                                                                                                                                                                                                                                                                   QQRSSYPFT 9
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SHITARA, N.,
SHITARA, N.,
VOSHJ
                                                                               KOIKE, MASAMICHI
SHITARA, KENYA
                                                HANAI, NOBUO
KUWANA, YOSHIHISA
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KOIKE, MASAMICHI
             HASEGAWA, MAMORU
PENTION: HUMANIZED ANTIBODIES
                                                                                                                 NAKAMURA, KAZUYASU
                                                                                                                                                                                                                                                                                                                    Conservative
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HASEGAWA, MAMORU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703)816-4000
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                                                                                                                                                                                                                                                                                                                                  93.8%;
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                                                                                                                                                                                                                                                                                                                                   Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                 Length 9;
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                                                               TELEFAX: (703)816-410 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                             SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                              TELECOMMUNICATION INFORMATION:
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STRANDEDNESS:
                                                                                            TELEPHONE:
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                                                                             (703)816-4100
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COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWAKE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-UN-96
CLASSIFICATION: TECOMPATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4100
TELEPAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFF 7----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                               STREET: 1100 NO.
CITY: ARLINGTON
STATE: VIRGINIA
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1100 NORTH GLEBE ROAD
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JENTION: HUMANIZED ANTIBODIES
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1; Mismatches
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RESULT 5
US-08-116-778E-2
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Best Local Similarity 88.
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                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                            OLECULE TYPE: protein
                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/116,778E FILING DATE: 07-SEP-93 CLASSIFICATION: 424
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
OTHER INFORMATION: /pi
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                                                                                                                                                                                                                                                                                                       LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                             NAME/KEY: sig_peptide
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                                                NAME/KEY:
OCATION: 49..55
[DENTIFICATION METHOD:
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(703) 816-4100
70 TO NO: 2:
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VENTION: HUMANIZED ANTIBODIES
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HANAI, NOBUO
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KOIKE, MASAMICHI
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24..33
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                                                                             D: BY SIMILARITY
D: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED D: CONSENSUS
/product= "HYPERVARIABLE REGION 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,955
                                                                                                                                                                                            BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN ESTABLISHED CONSENSUS
 BY SIMILARITY
WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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Pred. No. 2.5e+05
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Sequence 2, App. --
No. 5874255
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                                                                                                                                                                     TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/438,562
                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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                                                                                                    OLECULE TYPE: protein
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Local Similarity 88.9%;
les 8; Conservation
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CITY: ARLINGTON
STATE: VIRGINIA
IDENTIFICATION METHOD: IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                      LENGTH: 129 amino acids TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249
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                                                  NAME/KEY: sig_peptide
LOCATION: -22..-1
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(703)816-4100
- TN NO: 2:
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SHITARA, KENYA
HANAI, NOBUO
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MENTION: HUMANIZED ANTIBODIES
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BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN ESTABLISHED CONSENSUS
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                                                                                                                                                                                                                                                              249-76
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Pred. No. 0.15;
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US-08-483-528B-92
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                    TELEFAX: (703)816-410 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
                                         *OLECULE TYPE: protein
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IDENTIFICATION METHOD:
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LOCATION: 24..33
IDENTIFICATION METHOD:
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                                                                                                                                                                             FILING DATE: 0'CLASSIFICATION:
                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON STATE: VIRGINIA
NAME/KEY: sig_peptide
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                                                          TOPOLOGY:
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SHITARA, KENY
HANAI, NOBUO
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                                                         linear
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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Pred. No.
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US-09-393-385B-111
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                                                                      TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
                                                                                                                                                                                 SUPTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/393,385B
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                       TELECOMMUNICATION INFORMATION
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 22201-4714
                                           TYPE: amino acid
                                                                                                                                                             CLASSIFICATION:
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1100 NORTH GLEBE ROAD
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                                                         130 amino acids
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                                                                                                         (703)816-4100
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                          single
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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Pred. No. 0.15;
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Best Local Similarity
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                                                                                                                                           US-08-116-778E-37
                                                                                                                                                          RESULT 10
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                                                                                                Patent No. 5830470 GENERAL INFORMATION:
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                                                                                                                              Sequence 37,
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/393
FILING DATE: 27-JUN-96
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEPAX: (703)816-4100
                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: prote
                                                                     APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: HUMANIZED ANTIBODIES
                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
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                                                                                                                              Application US/08116778E
                                        NAKAMURA, KAZUYASU
KOIKE, MASAMICHI
SHITARA, KENYA
HANAI, NOBUO
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SHITARA,
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linear
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    Mismatches

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Pred. No. 0
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Pred. No.
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0.15;
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US-08-438-562-37
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         COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTION PATA:

APPLICATION NUMBER: US/08/438,562

FILING DATE: 10-MAY-95

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/116,778

APPLICATION NUMBER: 08/116,778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37; Application US/08438562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: NAKAMUI
APPLICANT: KOIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703)816-4100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
CLASSIFICATION: 424
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LENGTH: 133 amino acids
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TELECOMMUNICATION INFORMATION:
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NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                       APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                    STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 93.8%;
Local Similarity 88.9%;
                                                                                                                                                                                                                                                                                                        ADDRESSEE: NIXON & VANDERHYE P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 QQRSSYPYT 118
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1100 NORTH GLEBE ROAD
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HANAI, NOBUO
KUWANA, YOSHIHISA
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07-SEP-93
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ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARY J.

CLASSIFICATION:

REGISTRATION NUMBER:

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                                                          Best Local Similarity
Matches ' 8; Conserv
                                                                          Query Match
Best Local :
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                                                                                                                                                                                                         TELEFAX: (703)816-4100
NFORMATION FOR SEQ ID NO: 101:
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                 TOPOLOGY: 1i
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
CITY: A
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                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 8; Conserv
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                             1 QQRSSYPFT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: NIXON & VANDERHYE P.C.
FT: 1100 NORTH GLEBE ROAD
ARLINGTON
QQRSSYPYT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                 VIRGINIA
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                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOIKE, MASAMICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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88.9%;
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                                                                       Score 45; DB 2
Pred. No. 0.16;
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Pred. No. 0.
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RESULT 14
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08661052
                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                 APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
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SOCTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,507
FILING DATE: 02-Jul-1996
CLASSIFICATION: 530
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NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 11'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 703-816-4000
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OPERATING SYSTEM:
                                                                                     COUNTRY:
                                                                                                                             CITY: Boston
                                                                                                                                              STREET:
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1: USA
                                                                                                          Massachusetts
                                                                                                                                              60 State Street, Suite 510
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                                                                                           USA
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SYSTEM: PC-DOS/MS-DOS
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00 No. 5876691th Glebe Road, 8th Floor
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PC-DOS/MS-DOS
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Pred. No. 1
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1.2;
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RESULT 15
US-09-188-082-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-75941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                FILING LATE:
ATTORNEY/AGENT INFORMATION:
ANTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
TNFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.5%;
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
               TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/188,082
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APPLICATION NUMBER: 08/661,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
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CURRENT; APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
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CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Arnold, Beth E. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                 FILING DATE:
FOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 553;
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; MOLECULE TYPE: protein
US-09-188-082-16

Query Match
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSSYPLT 507
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Search completed: July 30, 2003, 09:38:30 Job time : 2.90033 secs

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Post-processing: Minimum Match 0%
Maximum Match 10
Listing first 45
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
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seq length: 2000000000
     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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   93.1
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                                                           GenCore version 5.1.6 (c) 1993 - 2003 Compugen
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S25174
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Ig heavy chain pre
Ig heavy chain V r
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                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <MON>
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S25174
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A36025
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Best Local
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Regult No.

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Minimum DB Maximum DB

Database

Searched:

Sequence:

	45	44	3	42	41	40	39	38	37	36	35	34	33	32	31	30
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	54.5	55.4	55.4	55.4	56.4	56.4	56.4	56.4	56.9	57.4	57.4	58.4	58:4	58.4	58.4	59.4
	99	127	126	107	171	120	115	110	98	118	114	116	98	97	86	136
	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
	C37262	S34014	I44151	A27646	S23623	S31999	S03482	PH1670	S26911	PH1666	PH1667	S24289	S26921	S16028	S29544	S31600
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Ig heavy chain V region - mouse (Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change (C;Accession: S25174; S33133 R;Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, submitted to the EMBL Data Library, July 1992 A;Description: Structure and binding properties of monoclonal ant A;Description: Structure and binding properties of monoclonal ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A36025;
A;Accession: A36025
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-82 <CAT>
A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
A;Accession: S33133
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: clone PR8-21
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: E36025
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 19-82 <CA2>
A;Cross-references: GB:M57273; NID:g194963; PIDN:AAA38116.1; PID:g194964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (pR8-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change
C;Accession: A36025; E36025
                                                                                                                                          A; Reference number: S25174
A; Accession: S25174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M55999; NID:g194955; PIDN:AAA38112.1; PID:g194956
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Pred. No. 6e-08;
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                                                                                                                                                                                                                                                                                 #text_change 21-Jan-2000
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A;Residues: 1-118 <MO2>
A;Cross-references: EMBL:X67622;
C;Superfamily: immunocionali
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C;Keywords: hete
F;15-98/Domain:
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A;Accession: $04576
A;Molecular analysis of the murine lupus-associated anti-self response:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
RESULT
                                                                                                                                                                                                                                                                                                                                                A; Accession: S15672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000 C;Accession: S04576
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A; Residues: 1-136 < KOF>
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                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                 Cross-references: EMBL:X58835; NID:g51978; PIDN:CAA41644.1; PID:g51979; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                          Residues: 1-116 <TEM>
                                                                                                                                                                                                                                                                                                                          Status: preliminary; nucleic acid sequence not
                                                                                                                                                                                                                                                                                                                                                              io/Technology 9, 266-271, 1991
;Title: Reshaping a human monoclonal antibody to inhibit human
;Reference number: S15672; MUID:91337412; PMID:1367535
                                                                                                                                                                                                                                                                                                                                                                                                                       Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
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                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                            Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S15672
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Best Local
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                                                                                                                                                                                                             immunoglobulin homology <IMM>
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                                                                                                                                     Conservative
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82.4%;
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Pred. No. 7.3e-06;
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Pred. No. 4.2e-06;
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Pred. No. 1.7e-06;
                                                                                                                                Mismatches
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    mouse (fragment)

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RESULT 7
E37262
Ig heavy chain V region (6H2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991
                                                                                                                                                                                                                                                                                                                                      C;Keywords: heterotetramer; immunoglobulin; pyroglutamic F;1-15/Domain: signal sequence #status predicted <SIG>F;16-143/Product: Ig heavy chain V-I region (Nd) #status
                                                                                                                                    문
                                                                                                                                                                     S
                                                                                                                                                                                                                                                                               F;30-113/Domain: immunoglobulin homology <IMM>F;16/Modified site: pyrrolidone carboxylic acid F;37-111/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 14q32.33-14q32.33
C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Cloning and sequence determination of the gene A,Reference number: A93933; MUID:83065234; PMID:6815656 A,Accession: A93933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;34-115/Domain: immunoglobulin homology <IVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S52445
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November
A;Description: Specific amplification by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:IGHV@
A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A94418
A; Contents: annotation; pa:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H. in Immediate Hypersensitivity: Modern Concepts and Developments,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-143 < KEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-137 < BER >
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76.5%;
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#text_change
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26938
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups
A;Reference number: S26885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000 C;Accession: S54912
R;Tomlinson, M.; Walter, G.; Cook, X.Y.Z.; Winter, G. submitted to the EMBL Data Library, November 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M57991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: E37262
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                    A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin bomology C;Keywords: heterotetramer; immunoglobulin
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A;Residues: 1-86 <TOM:
A;Cross-references: EMBL:Z18904; NID:g840779; PIDN:CAA79341:1; PID:g840780
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;3-86/Domain: immunoglobulin homology <IMM>
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A; Accession: S54912
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A; Residues: 1-98 < TOM>
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Best Local S
Matches 11
                                        Query Match
Best Local S
Matches 10
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10; Conserv
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WIDPENGDSDYAPKFQG 17
                                                                                                                                   immunoglobulin homology <IMM>
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58.8%;
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                                        Score 63; DB 2;
Pred. No. 0.0066;
4; Mismatches
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Pred. No. 0.004;
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Pred. No. 0.0013;
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RESULT 10
S26912
                                        R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1013
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D37262
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26912
                                                                                                                                                         Ig heavy chain V region (clone 111.67) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change C;Accession: PH1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M57990; NID:g195046; PIDN:AAA63328.1; PID:g195047
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A; Residues: 1-99 <GOS>
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A; Residues: 1-98 < TOM>
A;Status: nucleic acid sequence not shown A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region
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nilarity 68.8%;
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58.8%;
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Pred. No. 0.0066;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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0.0067;
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                                                                                             of clonally selective
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antiger

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A; Residues: 1-107 <TIL>
A; Experimental source: B cell, strain [NZB x NZW] F1 C; Superfamily: immunoglobulin V region; immunoglobulin C; Keywords: heterotetramer; immunoglobulin F; 15-98/Domain: immunoglobulin homology <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: immunoglobulin V region; immuno
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                 R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity A;Reference number: S31585
                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar_1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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S31680
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A; Residues: 1-108 <TIL>
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                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Tillman,
                                                                                                                                            Superfamily: immunoglobulin V region; immunoglobulin homology;Keywords: heterotetramer; immunoglobulin;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                           Molecule type: mRNA; Residues: 1-117 <CUI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Experimental source: B cell, strain [NZB x NZW]F1
;Superfamily: immunoglobulin V region; immunoglobulin homology
;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exp. Med. 176, 761-779, 1992
Title: Both IgM and IgG anti-DNA antibodies
Reference number: PH0971; MUID:92381444; PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y heavy chain V region (clone 17p.73) - mouse (fragment)
Species: Mus musculus (house mouse)
                                                                         Matches
                                                                                        Query Match
Best Local
                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                Status: preliminary
                                                                                                                                                                                                                                                                                                                   Accession: S31680
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Best Local (
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Best Local :
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69 WINDUSGGTNYAQKFQG
                          1 WIDPENGDSDYAPKFOG
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58.8%;
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88
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                                                                     Score 63; DB 2;
Pred. No..0.0081;
4; Mismatches
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Pred. No. 0.0074;
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Pred. No. 0.0073;
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PMID:1512540
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A;Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832 R;Olee, T.; Lu, B.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; J. Exp. Med. 175, 831-842, 1992 A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid A;Reference number: $23623; MUID:92156804; PMID:1740665 A;Accession: $23625
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S18551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Shin, B.K.; Matsuda, F.; N
EMBO J. 10, 3641-3645, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region precursor (VI-2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                           F;1-19/Domain: signal sequence #status predicted F;20-117/Product: Ig heavy chain V region (VI-2)
                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-117 < OLE>
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A; Residues: 1-117 <SHI>
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Job time
                       Search completed: July 30, 2003,
                                                                                                                                                                                                                                                                                                   F;34-117/Domain: immunoglobulin homology
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6.02658 secs
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58.8%;
                                                                                                    85
                            09:44:10
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Pred. No. 0.0081;
                                                                                                                                                                                                    Mismatches
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#status predicted
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Maximum Match 100%
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Maximum DB seq length: 200000000
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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101
1 WIDPENGDSDYAPKFQG
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 SwissProt_41:*
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 GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
SN HÜMAN
HVIZ MOUSE
HVIJ MOUSE
HV52 MOUSE
HV52 MOUSE
HV52 MOUSE
HV53 NEUCR
CHS2 NEUCR
FV03 MOUSE
YIGB ECOLI
C772 SOLME
HV03 MOUSE
YIGB ECOLI
G772 SOLME
HV05 MOUSE
HV07 MOUSE
HV08 MOUSE
HV06 MOUSE
HV60 MOUSE
HV
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HV1B_HUMAN
HV1B_HUMAN
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 P53214
P53214
Q11150
P01750
P06329
P06329
Q9hmV65
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Q14162
O14490
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             homo sapien
homo sapien
rattus norv
homo sapien
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CONFLICT NON TER SEQUENCE

125 M 147 16491 MW;

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948F9F72A5366C20 CRC64;

Query Match Best Local Similarity Matches 10; Conserv

Conservative

67.3%; Score 68; DB 1; Le: 58.8%; Pred. No. 0.00087; ... Mismatches 2;

Length 147; Indels

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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-wHC.
InterPro; IPR003596; Ig_v.
PEam; PF00047; Ig; 1.
SMART; SM00406; IG; 1.
SMART; SM00406; IG; 1.
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HUMAN
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21-JUL-1986 (Rel. 01, Last sequence upda
15-SEP-2003 (Rel. 42, Last annotation up
Ig heavy chain V-I region HG3 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HV1G
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EMBO J. 7:1047-1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsuda F., Lee K.H., Nakai S., Ohno H., Fukuhara S., Honjo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=88296408;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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SIMILARITY: Contains 1 immunoglobulin-like domain.
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  Chordata;
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Craniata; Vertebrata;
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28-FEB-2003
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NON TER
SEQUENCE
                                         Scharenberg A.M.; "ADP-ribose gating of the calcium-permeable Nudix motif homology.";
                                                                                                                       TISSUE-Spleen;
MEDLINE=21279171; PubMed=11385575;
MEDLINE=21279171; Pleiq A., Dunn C.A.,
                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP-ribose pyrophosphatase (EC 3.6.1.13) (ADP-ribose diphosphatase)
(Adenosine diphosphoribose pyrophosphatase) (ADPR-PPase) (ADP
Nature 411:595-599(2001)
                                                                                                      Perraud A.-L., Fleig A.,
Schmitz C., Stokes A.J.,
                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
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PIR; A02024; HVHUHG.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Rechavi G., Ram D., Glazer L., Zakut R., Givo
Merolutionary aspects of immunoglobulin heavy
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SIMILARITY: Contains
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3; PS50835; IG_LIKE; 1.
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ontains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
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                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                      Bessman
                                                                                                      Bagley L.A.,
ssman M.J., P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350
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0.33;
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                                                                                                           Penner
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                                                                                                                             Launay P.,
                                                                channel revealed by
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rohas S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Altsland D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length
""Generation and initial analysis of more than 15,000 full-length
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Best Local S
Matches 7
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TISQUE=Brain;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=27088257; Peingold E.A., Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase.
DOMAIN
                                                                                                                                            SN_HUMAN STANDARD; PRT; 1709 AA.
Q9EZZ; Q96DL4; Q9GZS5; Q9H1H6; Q9H1H7; Q9H7L
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Sialic acid binding Interpretation of the sequence of the sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8888
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EMBL; BC000542; AAH00542.1; -.
Genew; HGNC:8056; NUDT9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- CATALYTIC ACTIVITY: ADP-ribose + H(2)0 = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
      Eukaryota;
Mammalia; l
                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0005622; C:intracellular; NAS.
GO:0005622; C:intracellular; NAS.
GO:0019144; F:ADP-sugar diphosphatase activity; NAS.
GO:0005227; F:calcium activated cation channel activity;
GO:0006812; P:cation transport; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphate.
TISSUE SPECIFICITY: Ubiquitous.
SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. NUDF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   110
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PF00293; NUDIX; 1.
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   Eutheria;
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39125 MW;
   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.5%;
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Pred. No. 1.1;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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; 2EA5B24B88FB3420 CRC64;
   Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                   09H7L7;
Vertebrata; Euteleostomi; i; Hominidae; Homo.
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bailey J., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G.P., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G.P., Carter N.P.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Mickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Mickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Mickerson T.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Swann R.M., Sycamore N., Taylor R., Teore L., Thomas D.W., Thorpe A.,
RA Wilming L., Whittaker P., Williem S.A., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rocers J., Tromans A.C., Vaudin M., Wall M., Wallis JM.,
                                                                                                                                                                                                                  Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohi Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y., Matsumura Y., Moriya S., Chiba E., Momiyama H., Chogawa S., Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R., Kiga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y. Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y., Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Watanatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Sakine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Sekine M., Kikuchi H., Kanda K., Wagatsuma A., Kawaka Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawaka Suzuki Y., Sugano S., Wajahari K., Masuho Y., Nagai K., Isogai
                              "NEDO human cDNA sequencing project.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: Macrophage-restricted adhesion molecule that mediates sialic-acid dependent binding to lymphocytes, including granulocytes, monocytes, natural killer cells, B-cells and CD8 T cells. Preferentially binds to alpha2,3-linked sialic acid (By similarity). Binds to SPM/CD43 on T-cells (By similarity). May play a role in hemopoiesis.

-I-SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and
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Hattori A., Okumura K., Na
"Thereforization of long
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Blood 97:288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21638749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         rissum=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NA sequence and comparative 414:865-871(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7:357-366 (2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11214971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of human sialoadhesin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11133773;
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ng cDNA
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clones from human adult
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SMART; SM00408; IGC2; 4. PROSITE; PS50835; IG_LIKE; 14
Cell adhesion; Lectin; Antiger
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                                                                                                                                                                                                                             Immunoglobulin SIGNAL
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003005; Ig_MHC.
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GO:0005530;
GO:0016337;
GO:0007160;
GO:0006954;
                                                                                                                                                                                                                                                                                                                                                                               new; HGNC:11127; SN.; 600751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed by macrophages in various tissues.
High levels are found in spleen, lymph node, perivascular macrophages in brain and lower levels in bone marrow, liver kupffer cells and lamina propria of colon and lung. Also express further tries by inflammatory macrophages in rheumatoid arthritis.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBBRANILY.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 1 immunoglobulin-like (2-type domains).
DATABASE: NAME=PROW; NOTE=PROW 2:18-22(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/985165905 g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=3; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                           AK057560;
Q62230; 10
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AK024459;
AK024479;
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AL109804;
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domain;
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; CAC17543.1; -.
; CAC17542.1; -.
; BAB15752.1; -.
; BAB15749.1; -.
; BAB15769.1; -.
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P:cell-matrix adhesion; NAS.
P:inflammatory response; NAS
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BAB71527.1;
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Repeat; 1
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EXTRACELLULAR
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V-TYPE.

C2-TYPE
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SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
MEDLINE=83075344; PubMed=6816276;
MEDLINE=83075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
HOOD L.E.;
"Complete amino acid sequence of a mouse mu chain: homology among
heavy chain constant region domains.";
Biochemistry 21:5415-5424(1982).
                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                             HV12 MOUSE STANDARD; PRT; 117 AA
201756;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region MOPC 104E.
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QSMGENSVEMARQKETTQLIDEDAATCETSTCAPPLG ->
GEGRGLHLPGHSAQKPSS (in isoform 2).
/FIId=VSP 002571.
RRRRVCKQSMGENSVEMAFQKETTQLIDPDAATCETSTCAP
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K -> R (in dbSNP
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NL (in isoform 3).
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Sciurognathi; Muridae; Murinae; Mus
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InterPro; iPR0047; ig; 1.
Pfam; PF00047; ig; 1.

R SMART; SM00406; IGv; 1.
In Like; 1.

RW Immunoglobulin V region; Glycoprotein.
RW Immunoglobulin V region; Glycoprotein.
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PT DOWAIN 2 96 BY SIMILARITY.
PT SULFID 22 96 BY N-LINKED (GLCNAC. . .)
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SMARF; SS50835; IG LIKE; 1
PROSITE; PS50835; IG LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
                                                                                               DISULFID NON_TER
                                                                                                                                                                                                                                                                                                                   MEDLINE=80078170; PubMed=6765983; Schilling J., Clevinger B., Davie
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V reg
                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region J558.
                                                                                                                                                                                                                                                                                           Schilling J., Clevinger B., Davie J.M., Hood L.; "Amino acid sequence of homogeneous antibodies to dex rearrangements in heavy chain V-region gene segments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A02039; MHMS4E.
HSSP; P01789; 1MCP.
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                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                  Nature
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                               nterPro;
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                                                                                                                                                                                                                              SIMILARITY: Contains 1
                                                                                                                                                                                                                                         MISCELLANEOUS: THIS PROTEIN BINDS
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PROTEIN HAS AL
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; P01789; 1MCP.
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                                         Similarity
8; Conser
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           IDPENGDSDYAPKFQG
INPNNGGTSYNQKFKG
                                                                                                                                                                      IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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117
117
                                          Conservative
                                                                                    ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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THIS PROTEIN BINDS DEXTRAN
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Rodentia;
                                                                                    13024 MW;
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Pred. No.
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BY SIMILARITY
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                                                                                    292E2AF4BE447E41 CRC64;
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Best Local S
Matches 8
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P06330;
01-JAN-1988
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NON_TER
SEQUENCE
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P06327;
01-JAN-1988
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01-JAN 1999 (Rel. 38, Last annotatio
15-JUL-1999 (Rel. 38, Last annotatio
Id heavy chain V region VH558 A1/A4
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DOMAIN
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unrearranged VH gene segments."; Cell 40:271-281(1985).
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                                                                                        Mus musculus (Mouse)
                                                                                                        01-JAN-1988 (Rel. 06, Cr
01-JAN-1988 (Rel. 06, La
15-JUL-1999 (Rel. 38, La
Ig heavy chain V region
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=85099340; PubMed=2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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8; Conser
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an email to license@isb-sib.ch).
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nilarity 47.1%;
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06, Last sequence update)
38, Last annotation updat
region AC38 205.12.
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BY SIMILARITY.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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SEQUENCE

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RESULT 10
PUR4_ARATH
                 SQ STITE
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A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
A. Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
A. Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
A. Chung M.K., Conn L., Conway A.B., Conway J.-D., Fong B., Fujii C.Y.,
A. Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
A. Lin E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
A. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
A. Kim C.J., Koo H.L., Kremenetakaia I., Kurtz D.B., Kwan A., Lam B.,
A. Kim C.J., Koo H.L., Kremenetakaia I., Kurtz D.B., Kwan A., Lam B.,
A. Kim C.J., Koo H.L., Kremenetakaia I., Kurtz D.B., Kwan A., Lam B.,
A. Kim C.J., Koo H.L., Kremenetakaia I., Kurtz D.B., Kwan A., Lam B.,
A. Kim C.J., Koo H.L., Kremenetakaia I., Kurtz D.B., Kwan A., Lam B.,
A. Kim C.J., Koo H.L., Kremenetakaia I., Kurtz D.B., Kwan A., Lam B.,
A. Kim C.J., Koo H.L., Kremenetakaia I., Kurtz D.B.,
A. Kim C.J., Koo H.L., Kremenetakaia I., Kurtz D.B.,
A. Kim C.J., Pham P.K., Rizzo M., Narziali A.,
A. Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
A. Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
A. Sakano H., Tallon L.J., Tambunga G., Torium M.J., Town C.D.,
A. Sun H., Tallon L.J., Tambunga G., Torium M.J., Town C.D.,
A. Wu D., 'Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 8
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
28-FEB-2003 (Rel. 4
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NON TER
SEQUENCE
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
Probable phosphoribosylformylglycinamidine synthase, chloroplast
precursor (EC 6.3.5.3) (FGAM synthase) (FGAMS) (Formylglycinamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=84182519; PubMed=6201362;

Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

"A V region determinant (idiotope) expressed at high frequency in the second second
                                                                                              "Sequence and thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia;
MEDLINE=21016719; PubMed=11130712;
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                    Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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PIR; A02040; MHMS38.
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CATALYTIC ACTIVITY: ribosyl)glycinamide
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8; Conserv
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PS50835; IG LIKE;
bbulin V region.
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105
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Ig_MHC.
Ig_v.
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50.0%;
           ATP + N(2)-formyl-N(1)-(5-phospho-D-
+ L-glutamine + H(2)O = ADP + phosph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEGMENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
           phosphate +
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                    01-FEB-1995
01-FEB-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP BIND
ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Purine biosynthesis; Ligase; Chloroplast; Transit peptide. TRANSIT
                                                                                                                 in Schizosaccharomyces pombe polynucleotide ligases."; Proc. Natl. Acad. Sci. U.S.A
                                                                                                                                       "Covalent catalysis in nucleotidyl transfer reactions: motifs in Saccharomyces cerevisiae RNA capping enzymes in Schizosaccharomyces pombe and viral capping enzymes
                                                                                                                                                                          MEDLINE=95083638; PubMed=7991582; Shuman S., Liu Y., Schwer B.;
                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
mRNA capping enzyme alpha subunit (mRNA guanylyltransferase)
(EC 2.7.7.50) (GTP--RNA guanylyltransferase) (GTase).
CEG1 OR PCB1 OR SPBC2F12.08C.
                                                                                                                                                                                                                                                                                                                                                                     MCE1
                                                                                                                                                                                                                                                                                                                                                                                SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>:</del>
           MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A.,
                                  SEQUENCE FROM N.A.
STRAIN=972;
                                                                      Submitted
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     Schizosaccharomyces.
                                                                                                                                                                                                                                                 Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                 Fresco
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                         P40997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                             11
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SUBCELLULAR
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (formamido)-N(1)-(5-phospho-D-ribosyl)acetamidine PATHWAY: De novo purine biosynthesis; fourth step. SUBCELLULAR LOCATION: Chloroplast (Probable).
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                                                                                                                                                                                                                                                                                                                                                                     SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                              448 IDASNGASDYGNKF
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                                                                              L.D.,
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                                                                    (DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000728; AIRS_related
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1215
1387
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                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG52403.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contains 1 type-1 glutamine amidotransferase domain
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1215
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64.3%;
 Hayles
                                                                    Buratowski S.;
to the EMBL/GenBank/DDBJ
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).
GATASE (BY SIMILARITY)
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                                                                                                                   91:12046-12050(1994)
                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Lyne M., I
S., Basham
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                                                                      databases
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Lyne
m D.,
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re conserved
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            Stewart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration
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            Α.,
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RESULT 12
CHS2 NEUCH
ID CHS2
AC P3058
DT 01-AF
DT 01-FE
DT 01-FE
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RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gencles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Moneyd S., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Squares D., Seeger K., Sharp S.,
RA Kutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Raylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Galton J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Frosburg S.L.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Spakovski G.V., Ussery D., Barrell B.G.,
Nurse P.,
RA Spakovski G.V., Ussery D., Barrell B.G.,
O GTP TO THE S'END OF M-RNA CAPPING. TRANSFER OF THE GMP MOIETY
CC OG GTP TO THE S'END OF RNA YIELDING A 52 kDa ENZYME-GMP COVALENT
CC OG GTP TO THE S'END OF M-RNA CAPPING. TRANSFER OF
                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches
    01-APR-1993
01-FEB-1996
01-FEB-1996
                                                                 CHS2 NEUCR
P30589;
                                                                                                             NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U16143; AAA64996.1; -. EMBL; U18811; AAA58715.1; -. EMBL; Z97211; CAB10156.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001339; mRNA_cap_enzyme.
Pfam; PF03919; mRNA_cap_C; 1.
Pfam; PF01331; mRNA_cap_enzyme; 1.
Transferase; NucleotidyItransferase; mRNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GeneDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G(5') PPP-pur-mRNA.

GUBUNIT: THE M-RNA CAPPING ENZYME IS COMPOSED OF TWO SEPARATE CHAINS ALPHA AND BETA, RESPECTIVELY A MENA GUANYLYLTRANSFERASE AN RNA 5'-TRIPHOSPHATASE (BY SIMILARITY).

SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE EUKARYOTIC GTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T40133; T40133
                                                                                                                                                                                              260
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                                                                                                                                                                                                                                                                                                                                                         protein.
E 67
E 67
E 402 AA
                                                                                                                                                                                                                                                                            Similarity 9; Conser
                                                                                                                                                                                         PEEGDIDYSAMPEFQ 274
                                                                                                                                                                                                                 PENGDSDYA--PKFQ
(Rel. 25, Created)
(Rel. 33, Last sequence update)
(Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                             ΑA,
                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                             46875
                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                              43.6%;
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                                                                                                                                                                                                                                                                                                                                                             WW;
                                                                                                                                                                                                                                                                            <u>۷</u>
                                                                                                                                                                                                                                                                                              Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                 GUANYLYLATION SITE,
K->A: LOSS OF FUNCT
                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                             76B1E2052DABB974 CRC64;
                                                                                                                                                                                                                                                                               Mismatches
                                                                                       944
                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                   OF FUNCTION
                                                                                       AA
                                                                                                                                                                                                                                                                                                                    Length 402
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA capping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL outstation
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RESULT 13
HV03_MOUSI
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Best Local S
Matches 8
                                           MOUSE
HV03 MOUSE
p01747;
21-JUL-1986 (Re:
21-JUL-1986 (Re:
15-SEP-2003 (Re:
15 Peavy Chain )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurospora crassa.
Eukaryota; Fungi; As
Sordariomycetidae; S
NCBI TaxID=5141;
                                                                                                                                                                                                                                                                                               TRANSMEM.
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EMBL; M82951; AAA33582.1; -.
PIR; B45189; B45189.
PIR; T47246; T47246.
                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                  Transferase;
Multigene fa
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Din A.B., Yarden O.;
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CHS-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92115692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 250-438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microbiology 140:2189-2197(1994).
                                                                                                                                                                                                                                                                                                                       TRANSMEM
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Pfam; PF01644; Chitin_synth; 1.
ProDom; PD002998; Chitin_synth; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucosaminyl) (N+1). SUBCELLULAR LOCATION: Integral SIMILARITY: BELONGS TO THE CHIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. Natl. Acad. Sci. U.S.A. 89:519-523(1992).

FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.

CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + {(1,4)-(beta-D-glucosaminyl)}(N) = UDP + {(1,4)-(N-acetyl-beta-D-glucosaminyl)}(N)
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T47246; T47246.
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8; Conserv
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ain V region
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15-JUL-1998 (Rel. 36, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Hypothetical protein yigh.
YIGB OR B3812 OR SF3890.
MEDLINE=91072248; PubMed=2254268; Colloms S.D., Sykora P., Szatmari G., Sher "Recombination at ColE1 cer requires the E product, a member of the lambda integrase
                                                                                                              MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D
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NON_TER
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Eur. J. Immunol. 12:1023-1032(1982).
-i- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED
                                                SEQUENCE FROM N.
SPECIES=E.coli;
                                                                                  Science
                                                                                                                                                                                                      Daniels D.L., Plunkett G. III, Burland V.II", Marland V.II", Marlysis of the Escherichia coli genome: from 84.5 to 86.5 minutes.";
Science 257:771-778(1992).
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. SPECIES=E.coli; ST
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Immunoglobulin V region; Hybridoma
DOMAIN 1 111 IG-LI
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                                                                                                          Mau B.,
                                                                                                                                                                     SPECIES=E.coli;
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                                                                                                                                                                                                                                                    SPECIES=E.coli; STRAIN=K12 / MG1655; MEDLINE=92358234; PubMed=1379743;
                                                                                                                                                                                                                                                                                                               Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                     Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                 Escherichia coli, and
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SMART; SM00406; IGv
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InterPro; IPR007110;
InterPro; IPR003006;
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SEQUENCE FROM N.A.
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                                                                                  complete genome sequence nce 277:1453-1474(1997).
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13307 MW; FF04E4A167B654AF CRC64;
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RESULT 15
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                                                                                                                                                                                                                                                      InterPro; IPR006433; HAD SF A v1.
InterPro; IPR005834; Hydrolase.
Pfam; PF00702; Hydrolase; 1.
TIGR01549; HAD SF-IA-v1; 1.
Hypothetical protein; Complete proteome.
CONFLICT 13 13 L -> V (IN REF. 1)
CONFLICT 200 200 S-> T (IN REF. 1)
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EMBL; AE000457; AAC76815.1; --
EMBL; M8257; AAA24764.1; --
EMBL; X00738; -; NOT ANNOTATED CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SPECIES=S.flexneri; STRAIN=301 / Serot
MEDLINE=22272406; PubMed=12384590;
MEDLINE=22272406; Yu J., Wang Y., Shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Transcription of the uvrD gene of Escherichia the lexA repressor and by attenuation."; Nucleic Acids Res. 11:8625-8640(1983).
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EcoGene; EG11202; yigB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Shigella flexneri 2a: insights into through comparison with genomes of Escherichia coli K12 Nucleic Acids Res. 30:4432-4441(2002).
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Finch P.W., Emmerson
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h P.W., Emmerson P.T.;
nucleotide sequence of the uvrD gene
eic Acids Res. 12:5789-5799(1984).
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7; Conserva
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EMBL; X71655; CAA50646.1; -.

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InterPro; IPR001128; Cytochrome_P450.

Pfam; PF00067; p450; 1.

Pfam; PF00067; p450; 1.

PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME_P450; 1.

Oxidoreductase; Monooxygenase; Heme; Multigene family.

Oxidoreductase; Monooxygenase; Heme; Multigene family.
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STRAIN=CV. Sinsadoharanasu; TISSUB=Hypocotyl;

MEDLINE=9413942; PubMed=8307197;

Toguri T., Tokugawa K.;

"Cloning of eggplant hypocotyl cDNAs encoding cytochromes P450 belonging to a novel family (CYP77).";

FEBS Lett. 338:290-294(1994).

-i- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Solanaceae; Solanum.
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43.8%; Pred. No.
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Perfect score:
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sp_virus:*
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sp_unclassified:*
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Q8vcv5 mus
Q9u192 homo
Q8ncb9 homo
Q96kb3 homo
Q8nbn1 homo
Q8k1j4 mus
Q8bvu5 mus
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Q96ga6 homo
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4			16	44.6	45	φ
Q9f8n0 carboxydoth	2 Q9F8N0		138	44.6	45	æ
Q9z1c4 mus musculu			11	45.0	45.5	7
Q9ji04 rattus norv			173	45.5	46	თ
Q8pjj7 xanthomonas			145	45.5	46	G
Q8gal9 arthrobacte	o		66	45.5	46	4
Q96qs0 homo	ø		159	45.5	46	ω
Q9qxf0 mus			11	45.5	46	N
Q9qxe9 mus	11 Q9QXE9		11	45.5	46	_
Q921t2 mus			52	46.5	47	0
Q91wt1 mus	11 Q91WT1		48	46.5	47	v
Q8ng25 homo	Q8NG25	0 4	35	46.5	47	œ
Q8ng26 homo	Ö		30	46.5	47	7
Q8cxi6 oceanobacil	Ó		643	47.5	48	σ
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Q99la6 mus musculu	11 Q99LA6		48	47.5	48	4
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Q9sts2 arabidopsis			323	47.5	48	٥
Q925s3 mus			147	47.5	4.8	w
Q9j179 mus			102	47.5	48	ω
Q8r3h6 mus	.1 Q8R3H6	4	47.	48.0	48.5	7

ALIGNMENTS

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RESULT 1

Q99L3

ID U31

ID Q99L

AC Q99L

AC Q99L

DT 01-J

DT 01-J

DT 01-M

Simi

OS Mus

OC Mamm

OX NCEIL

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OR SEQU

RA Stabu

DR HSSE

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RESULT 2
Q8WY24
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Best Local S
Matches 12
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Q99L31;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
   Q8WY24
                                                                                                                                                                                                                 Pfam; PF00047; ig; 3.

SMART; SM00406; IGv; I.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS00290; IG MHC; 1.

SEQUENCE 468 AA; 51661 MW;
                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                           1 WIDPENGDSDYAPKFQ 16
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12; Conservative
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   PRELIMINARY;
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75.0%;
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   PRT;
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RESULT 3
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01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
"Identification and characterization of SNC66, a Ig-like
down-regulated in colorectal cancer.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF283666; AAL36987.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047: io. 4
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01-DEC-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; BC009851; AAH09851.1; -. InterPro; IPR000005; HTHAraC.
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

SEQUENCE 497 AA; 53665 MW;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                               Hypothetical SEQUENCE 61
                                                                                                                                                                                                    PROSITE; PS00041; HTH ARAC FAMILY 1; PROSITE; PS50835; IG_LIKE; 5. PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
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Mammalia; Eutheria;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=B-cell;
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Primates;
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Primates;
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Pred. No.
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Ig-like
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RESULT 4
Q9J185
ID Q9J187
AC Q9J1
AC Q9J1
AC Q9J1
DT 01-Q
DT 01-Q
DT 01-W
DE Anti
DE FRANCE
CO MANN
OC MANN
OC NCBI
RN G11
RN G11
RN MEDI
RR MADI
RR MADI
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Matches 11
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Q9JL85;
01-OCT-2000
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NON_TER 1 1 1

NON_TER 109
                                                                                                                                                                             IgG4 monclonal antibody
inhibitor.";
Blood 92:496-506(1998).
                                   Pfam; PF00047; ig; SMART; SM00406; IG
                                                                                                                                     EMBL; AJ224083; CAJ
HSSP; P01772; 2FB4
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "T-Cell-dependent antibody response to the dominant streptococcal polysaccharide, N-acetyl-glucosamine, with cardiac myosin.";
                                                                                                                                                                                                                     Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VI:
IGG4 monclonal antibody derived from
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=98322155; PubMed=9657749;
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                          IGG VH protein precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999
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HSSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20448942; PubMed=10992488; Malkiel S., Liao L., Cunningham M.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                       IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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IPR003006; Ig_MHC.
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Rodentia;
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, Last annotation updat
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Pred. No.
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Sciurognathi; Muridae; Murinae; Mus
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PROSITE; Signal.

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IG_LIKE;

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01-MAY-2000
01-MAY-2000
01-MAR-2003
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NON TER,
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ol-MAY-2000 (TrEMBLrel. 13, Careated)
Ol-MAY-2000 (TrEMBLrel. 23, Last annotation update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
SEQUENCE FROM N.A.
MEDLINE=9827139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.
Young D.C.;
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Mammalia; Eutheria;
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[1]
                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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HSSP; P01810; 2FBJ
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                    P.L.,
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Pred. No.
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                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SMART; SM00409; IG; 3.

SWART; SM00407; IGc1; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS00299; IG MHC; 2.

SEQUENCE 480 AA; 51645 MW;
                                                           Q8VCV5;
Q8VCV5;
01-MAR-2002
01-MAR-2002
01-MAR-2003
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC029188; AAH29188.1; InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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HSSP; P01810; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies fetus.";
Clin. Immunol. Immunopathol. 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        в
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                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; IPR003599; Ig.
; IPR007110; Ig-like.
; IPR003597; Ig cl.
; IPR003006; Ig_MHC.
; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WIDPENGDSDYAPKFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50835;
                                                                                                                                                                                                                                                                                                                                                         WISPGDGSSEYNEKFKG
                                                                                                                                                                                                                                                                                                                                                                                                                 WIDPENGDSDYAPKFOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WINPNSWTTNYAOKFOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 AA;
                          (TrEMBLrel. 20, Cre
(TrEMBLrel. 20, Las
(TrEMBLrel. 23, Las
(152.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD56256.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG_LIKE;
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52.9%;
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52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
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                                                                                                                                 Created)
                                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; I
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87:184-192(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 480;
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Hypothetical

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RESULT 11
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Q9UL92
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Best Local S
Matches 9
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Best Local
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NON_TER
SEQUENCE
Q8NCB9
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
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01-MAY-2000
                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF035022; AAD56258.1; HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ol-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC018455; AAH18455.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fragment)
                                                                                                                                                                                                                                                                                                                                    PF00047; ig; 1.
; SM00406; IGv; 1.
TE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                            Similarity 9; Conserv
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                                                                                                                                       IDPENGDSDYAPKFQG 17
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                             4,
                                                                                                                                                                                                                                                                                  124
124 AA;
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PRELIMINARY;
                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                    13580 MW;
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                                                                                                                                                                                            2
                                                                                                                                                                                            Score 51; DB
Pred. No. 2.6;
2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; l
Catarrhini; Hominidae;
PRT;
                                                                                                                                                                                                                                                                                    1BAAACBD96ACD2A2 CRC64;
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300
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                                                                                                                                                                                                                DB 4;
2.6;
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B
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                                                                                                                                                                                                                                    Length 124;
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Homo.
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RESULT 12
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01-OCT-2002
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01-OCT-2002
01-MAR-2003
                                                                                                                                                        Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wishikawa M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Magatsuma M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Yatanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu T., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wayanagi T., "NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okamo K., Yoshikawa Y., Aotsuka S., Sasaki W., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; "NEDO human cDNA sequencing project."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                       Pfam; PF00293; NUDIX; 1.
Hypothetical protein.
SEQUENCE 350 AA; 3904
                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein FLJ14389.
Homo sapiens (Human).
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Mammalia; Eutheria;
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                                                                                                                                       InterPro; IPR000086; NUDIX_hydrolase.
                                                                                                                                                                                                                                                                                              TISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
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Primates;
                                                                                                        39042 MW;
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Pred.
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                                                                                                        8BE1A31ECCFB343D CRC64;
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OX NCB1
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RP SEQUI
RA STRAN
DR EMBL;
DR Pfam,
SQ SEQUI
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Q8BVU5
ID Q8BVU
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Q8BVU5;
01-MAR-2003
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Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033921; AAH33921.1; -.
InterPro; IPR000086; NUDIX_hydrolase.
Pfam; PF00293; NUDIX; 1.
SEQUENCE 350 AA; 38623 MW; 6FD9371307AB3366 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8K1J4
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Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Nagahari K., Sugano S., Isogai T.;

"HRI human cDNA sequencing project.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AK075408; BAC11601.1;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein NT2RP2002907.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to nudix (Nucleoside diphosphate linked moiety X)-type motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8K1J4;
Mus musculus (Mouse).
               Nudix.
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                                                                                            The FANTOM Consortium,
the RIKEN Genome Exploration Research Group
"Analysis of the mouse transcriptome based o.
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK076500; BAC36366.1; -
EMBL; AK076500; BAC36366.1; -
                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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Humanised antibody
VEGF antagonist an
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VEGF antagonist an
Antigen-binding pr
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Mouse anti-KDR plC
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AAU76632		w	(4)	AAY39543	AAY39542	AAY39541	AAY39540	AAY39539	AAY39538	AAY39537	AAY39536	AAY39530	AAY39528	AAR60566	AAR60565	AAY39531	ABJ26724	AAU74412	AAE25955	AAY97235	AAY70787	AAW89173	AAY70794	ABJ26719	AAU74407	AAE25950	AAY97230	16	ABJ26732	442	96	AAE25961	91	8270	AAE13145
Murine Col-1(CEA a	sed	ᇋ.			Murine	Murine	Humanised Murine C	Murine	Murine		Murine	ed Murine	Murine COL1 VH cha	Anti-carcinoembryo	~	Humanised Murine C	VEGF binding relat	Antigen-binding pr	Mouse anti-KDR p1C	_	anti-p5	7	ne anti		chair	Mouse anti-KDR p1C	Complementary dete	-p53 monoclon	ga 4	igen-bind	binding	ding immun	C11 vector h	tagonist a	Chimeric p1C11 hea

ALIGNMENTS

				PF 30-MAI		PN WO2001	OS Mus sp.					×			AC AAE13138;	ID AAE131	RESULT 1	
WPI: 2001-662942/76.	7 00.6	(IMCL-) IMCLONE SYSTEMS INC. (CORR) CORNELL RES FOUND INC.	31-MAR-2000; 2000US-0540770.	30-MAR-2001; 2001WO-US10504.	11-OCT-2001.	WO200174296-A2.	70.	Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.	lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;	tatic; heavy chain hypervariable region; VH; myelocytic leukaemia	lar endothelial growth factor receptor; VEGFR; antagonist; tumour		Humanised antibody murine heavy chain hypervariable region (VH) CDR2.	28-JAN-2002 (first entry)	138;	AAE13138 standard; peptide; 17 AA.		

Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -

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RESULT 2
AAB82704
ID AAB8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGER) in mammals particularly humans. The method involves treating the mammals with humanised VEGER monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody murine heavy chain hypervariable region (VH) CDR-2 used in the exemplification of the invention.
Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                                                                                                                                                                                                                                                                              IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disease; tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
                                                            WPr; 2001-514531/56
                                                                                                                                                                         28-JAN-2000; 2000US-0178791.
31-MAR-2000; 2000US-0539692.
                                                                                                                                                                                                                                                                                                                      Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                               colon carcinoma; ovarian carcinoma; neuroblastoma;
glioblastoma multiforme; melanoma; therapy; heavy chain; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB82704 standard; Peptide; 17
                                                                                                                                                                                                                         29-JAN-2001; 2001WO-US02839
                                                                                                                                                                                                                                                        02-AUG-2001
                                                                                                                                                                                                                                                                                       WO200154723-A1
                                                                                                                                                                                                                                                                                                                                     Chimeric
                                                                                                                                                                                                                                                                                                                                                                    complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGF antagonist antibody IMC-1C11 VH CDR-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
17; Conserv
                                                                                                                            IMCLONE SYSTEMS INC.
                                                                                                                                            SUNNYBROOK HEALTH SCI CENT
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mo sapiens.
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Pred. No. 5.3e-09;
; Mismatches 0;
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RESULT 3
AAU7416
ID AAU7
XX AAU7
XX ADU7
XX AAU7
XX AOU7
AC Comp
DE Heav
XX Comp
KW Angi
KW VEGF
KW Angi
KW VEGF
KW Angi
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XX SMus
XX WO20
PX 29-N
XX IM
PF 24-N
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PT two
PS Cla:
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The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent preventing significant toxicity of the chemotherapeutic agent and is especially molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma colon carcinoma prostate carcinoma, neuroblastoma multiforme or melanoma (all claimed).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                        WPI; 2002-106189/14.
N-PSDB; AAS20287.
                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity determining region; CDR; CDRH2; antigen; cytogtatic; angiogenesis inhibitor; vascular endothelial growth factor receptor; VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor; antibody heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of complementarity determining 2 of the heavy chain variable region (see also AAB82701) of IMC-IC11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The
                                                                                                                                                                                                                                  24-MAY-2000;
                                                                                                                                                                                                                                                                     24-MAY-2001; 2001WO-US16924.
                                                                                                                                                                                                                                                                                                        29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                         WO200190192-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU74416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU74416 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 37; 42pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complementarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               determining region
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Claim 59; Page 60; 64pp; English.

two polypeptides and

two

second polypeptides

comprises

för reducing complex of

New bispecific immunoglobulin-like antigen-binding protein tumour growth and for inhibiting angiogenesis, comprises a

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RESULT 4
ABJ26728
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Best Local S
Matches 17
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light chain constant domain (CL domain), and P2 has an antigen-binding
site located to the N terminus of the CHI domain. (I) is useful for:
neutralising the activation of a vascular endothelial growth factor
(VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
reducing endothelial cell proliferation; inhibiting angiogenesis;
reducing endothelial cells; blocking interaction of a protein and
its ligand; promoting interactions between immune cells and target cells;
and in vivo and in vitro for investigative, diagnostic or treatment
methods. The design of (I) provides for efficient production so that
substantially all of the antigen-binding proteins production so that
the desired configuration. (I) is bivalent and bispecific, homogeneous
and in tetrameric form. The heavy chain constant domains which constitute
the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
antibody and which provide other antibody functions can be present. There
is no requirement for processing in vitro to obtain the complete product.
This peptide sequence represents the heavy chain variable domain
complementarity determining region H2 (CDRH3) version #2 incorporated
into an antigen-binding represents in he method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; antibody; antigen binding site; leukaemia cell; vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABJ26728;
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                            New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bispecific antigen-binding protein; mouse; murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGF binding related peptide SEQ ID No 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2002; 2002WO-US20332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003002144-A1.
                                                                                                                                                                      WPI; 2003-201468/19.
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or for treating tumors -
                                                                                                                                                                                                                                                                                                            IMCLONE SYSTEMS INC
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Pred. No. 5.3e-09;
, Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth factor;
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밁 S

Claim 10;

Page

53; 98pp;

English

relates to a novel antibody having a first antigen binding

Hodgkin's

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ARESULT 5
AAE13143
ID AAE1
XX AAE1
XX AAE1
XX AAE1
XX AAE1
XX AAE1
XX VASC
XX Huma
XX VASC
XW Cyto
XW mono
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Best Local
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                      growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humansised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic hymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to
                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
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Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised antibody heavy chain fragment.
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DB; AAD21669.
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Pred. No. 5.3e-09;
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Chimeric
          The present sequence is that of the heavy chain variable region of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody
                                                                                    Treating or controlling an angiogenic dependent condition (e. neoplasm, collagen-vascular or autoimmune disease) in mammal administering a combination of an antiangiogenic molecule and
                                                                                                                                                                                                                           28-JAN-2000; 2000US-0178791.
31-MAR-2000; 2000US-0539692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune diseau tumour; breast carcinoma; lung carcinoma; prostate carcinoma; tumour; bracat carcinoma; carcinoma; neuroblastoma;
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                                                       Disclosure;
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Pred. No. 4.2e-08;
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                                                                                       antiangiogenic molecule and
anti-angiogenic
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the mentherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-106189/14.
N-PSDB; AAS20288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; angiogenesis inhibitor; tumour; leukae vascular endothelial growth factor receptor; VEGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody heavy chain variable domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
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Pred. No. 4.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukaemia; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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The invention describes an antigen-binding protein (1) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CI domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain (I) is useful for: neutralising the activation of a vascular endothelial growth factor

receptor;

reducing tumour

growth;

angiogenesis;

Claim 61; Page 60; 64pp; English.

New bispecific immunoglobulin-like antigen-binding protein tumour growth and for inhibiting angiogenesis, comprises a

for reducing complex of

two polypeptides and two second polypeptides

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RESULT 8
ABJ26729
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Best Local S
Matches 17
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The invention relates to a novel antibody having a first antigen bind site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; mouse; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 migration of human leukaemia cells; blocking interaction of a protein its ligand; promoting interactions between immune cells and target count in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that
                                                                                                                                                                                                                                                                                                                              New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABJ26729 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF binding
                                                                                                                                                                                                                                           Disclosure; Page 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-2001; 2001US-301299P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2002; 2002WO-US20332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003002144-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-201468/19.
DB; ABT23307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                  or for treating tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMCLONE SYSTEMS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                        98pp; English.
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Pred. No. 4.2e-08;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ein and cells;
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for investigative and

diagnostic

The present invention relates to novel immur to kinase insert domain-containing receptor mouse foetal liver kinase (FLK)-1 receptor)

vascular endothelial

growth

factor

immunoglobulin molecules that eptor (KDR) (a human homologue ptor) with an affinity comparat actor (VEGF) and that neutralis

an affinity comparable

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ARESULT 9
ARE25965
ID ARE25965
ARC ARE2
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAR', LIMMUNOGLODULIN; Kinase insert domain-containing receptor; KDR; foetal liver kinase; FLK-1 receptor; vascular endothelial growth fact VEGF; tumour growth; heavy chain variable region; VH; angiogenesis; plC11; scFv antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
                                                                                                                                                                                       Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparational vascular endothelial growth factor, and neutralizes activat
                                                                                                                                                                                                                                                                                                                                                                                                                      (ZHUZ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse anti-KDR plCll scFv antibody VH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE25965;
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                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                       Zhu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-2000; 2000US-0493539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001; 2001US-0976787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002064528-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                               2002-589175/63.
DB; AAD42832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
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                                                                                                                                                                                                                                                                                                                                                                                                                   ZHU Z.
WITTE L.
                                                                                                                                                                                                                                                                                                                                                                    Witte L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WIDPENGDSDYAPKFOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WIDPENGDSDYAPKFQG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determining region 3 (CDR-H3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Heavy chain complementarity
determining region 2 (CDR-H2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Heavy chain complementarity
letermining region 1 (CDR-H1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= Signal-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                      34pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mouse plC11 scFv antibody mature VH region"
                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
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Pred. No. 4.2e-08;
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RESULT 10
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Best Local
                  Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
 Example 3;
                                                                          WPI; 2001-662942/76
                                                                                                                                                      31-MAR-2000; 2000US-0540770
                                                                                                                                                                            30-MAR-2001; 2001WO-US10504
                                                                                                                                                                                                   11-OCT-2001
                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE13145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR plC11 scFv antibody heavy chain variable region (VH).
                                                                                                                                                                                                                      WO200174296-A2
                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric plCll heavy chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plC11 vector.
                                                                 AAD21682.
                                                                                                                      IMCLONE SYSTEMS INC. CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WIDPENGDSDYAPKFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIDPENGDSDYAPKFQG
                                                                                                 Rafii
 Fig 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
Unidentified.
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                                                                                                                                                                                                                                           sequence shown
119..125
/label= CDR_H3
                                                                                                                                                                                                                                                                                       sequence shown in
                                                                                                                                                                                                                                                                                                                                                                  /note= "Mature chimeric plC11 heavy chain fragment"
45..54
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                            note= "Residue 'O'
                                                                                                                                                                                                                                                                                                           note= "Residue
                                                                                                                                                                                                                                                                                                                                 'label= CDR_H2
                                                                                                                                                                                                                                                                                                                                                      'label= CDR_H1
                                                                                                                                                                                                                                                                                                                                                                                                  /label= Leader_peptide
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Pred. No. 4.9e-08;
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fig-11 of the specification"
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fig-11 of the specification"
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RESULT 11
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XW CUMO
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; anglogenesis; antiangiog antitumour; neoplasm; collagen-vascular disease; autoimmune tumour; breast carcinoma; lung carcinoma; prostate carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The methoder of the control of the contro
                                                                                                                                                    29-JAN-2001; 2001WO-US02839
                                                                                                                                                                                                                                   02-AUG-2001
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glioblastoma multiforme; melanoma; therapy; heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118.
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28-JAN-2000; 2000US-0178791. 31-MAR-2000; 2000US-0539692.

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RESULT 12
AAE28916
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, glioblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of the heavy chain variable region (IMC-IC11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibor or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or
                                                                                                                                                                                                         Human; tumour; vascular endothelial growth factor receptor; metastasis; epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC; breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                                                                                                                                     c-plC11 vector heavy chain (VH) protein.
                                                                                                                                                                                                                                                                                                       27-DEC-2002
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                                                                                                                                                                              Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136
                                                                                                                                                                                 Unidentified.
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                                                                                                                                                                sapiens.
                                                         /note=
45..54
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                                                                                                                                  Location/Qualifiers
                                       note= "CDR1"
                                                                                                   note= "Leader peptide"
              note= "CDR2"
                                                                                                                                                                                                                                                                                                                                                                 Protein; 136
                                                                                                                                                                                                                                                                                                       entry)
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (C) (NEGFR) antagonists in combination with radiation, chemotherapeutic agent, or epidermal growth factor receptor (EGFR) antagonists. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, small intestine, colon, spleen, bone, ckidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, colon earrow, blood, thymus, uterus, testicles, cervix or liver) over cexpresses VEGFR. It is also useful for inhibiting growth of colon tumour or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR. CC is preferably useful for treating subjects with both solid tumours, preferably high vascular tumours and non-solid tumours. The inhibition or reduction of tumour includes prevention or inhibition of the corresponding to the progression of tumours includes the invasiveness, metastasis, recurrence and increase in size of the tumour. The present sequence is created to illustrate the progression of the match of the tumour. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-691738/74.
N-PSDB; AAD46315.
                                                                              Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR; foetal liver Kinase; FIK-1 receptor; vascular endothelial growth factor; VEGF; tumour growth; heavy chain variable region; VH; angiogenesis; p1C11; scFv antibody.
                                                                                                                                                                                                 15-NOV-2002
                                                                                                                                                                                                                                  AAE25961;
                                                                                                                                                                                                                                                                 AAE25961 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of inhibiting tumour growth which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 9; Fig 19; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor
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                                              de sum
                                                                                                                                                                KDR binding immunoglobulin related mouse protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is used to
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                                                                                                                                                                                                                                                                                                                                                     WIDPENGDSDYAPKFOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101; DB 2
Pred. No. 5e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
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US2002064528-A1

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RESULT 14
AAE25963
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Best Local :
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     WPI; 2002-589175/63
                                                   (/ITIM)
                                                                                                                                                                                                                             Mouse;
                               Zhu Z,
                                                                                   28-JAN-2000; 2000US-0493539
                                                                                                        12-OCT-2001; 2001US-0976787
                                                                                                                               30-MAY-2002.
                                                                                                                                                    US2002064528-A1
                                                                                                                                                                                                       foetal liver kinase;
VEGF; tumour growth;
                                                                                                                                                                                                                                                  KDR binding
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                                                                                                                                                                                                                                                                                                                  AAE25963 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparal human vascular endothelial growth factor, and neutralizes activat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-589175/63.
N-PSDB; AAD42825.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
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                                                                                                                                                                                                     immunoglobulin; kinase insert domain-containing receptor; KD
liver kinase; FLK-1 receptor; vascular endothelial growth fa
tumour growth; heavy chain variable region; VH; angiogenesis;
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                                                    ZHU Z.
WITTE
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17; Conserv
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WITTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 AA;
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                                                                                                                                                                                              antibody
                                                                                                                                                                                                                                                  immunoglobulin related mouse
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Pred. No. 9e-08;
Mismatches
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WPI; 2002-106189/14

24-MAY-2000;

2000US-206749P

(IMCL-)

IMCLONE SYSTEMS INC

24-MAY-2001; 2001WO-US16924

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RESULT 15
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                          cell
                                                                                                                                                                                                                                                                                                                                                                                    Antigen-binding protein; single chain variable fragment; svFv, cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibod vascular endothelial growth factor receptor; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting the activation of KDR, for reducing tumour growth and for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU74420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU74420 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
                                                                                                                29-NOV-2001.
                                                                                                                                       WO200190192-A2
                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 17-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human vascular
KDR -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, single chain variable fragment version #2.
                                                                                                                                                           /note= "15 amino acid linker joins the VH
    regions of the single chain variat
    protein. Encoded by AAS20285"
                                                                                                                                                                                                                                                         118..132
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                          /label= VH
                                                                                                                                                                                   /label= VL
                                                                                                                                                                                                                                            /label= Linker
                                                                                                                                                                                                                                                                                                                                                                          inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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Pred. No. 9e-08;
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                                                                                                                                                                                                          le chain variable
AAS20285"
                                                                                                                                                                         domain. Specifically
                                                                                                                                                                                                                                                                                domain.
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                                                                                                                                                                                                                                                                                                                                                                                                          antigen;
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CC complex of two polypeptides (P1) and two second polypeptides (P2) which CC are stably associated in an immunoglobulin like complex. P1 has an CC antigen-binding site located to the N terminus of immunoglobulin (Ig) CC light chain constant domain (CL domain), and P2 has an antigen-binding CC site located to the N terminus of immunoglobulin (Ig) CC light chain constant domain (CL domain), and P2 has an antigen-binding CC sight chain constant domain (CL domain), and P2 has an antigen-binding CC sight proceed to the N terminus of the CH1 domain. (I) is useful for: CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; CC reducing endothelial cell proliferation, inhibiting vEGF induced CC migration of human leukaemia cells; blocking interaction of a protein and CC its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment CC methods. The design of (I) provides for efficient production so that the desired configuration. (I) is bivalent and bispecific, homogeneous can the desired configuration. (I) is bivalent and bispecific, homogeneous can the desired configuration. (I) is bivalent and bispecific, homogeneous can the terameric form. The heavy chain constant domains which constitute the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural CC is no requirement for processing in vitro to obtain the complete product. (scFv), an engineered protein containing a variable light and variable invertion.
                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides -
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 63; Page 62-63; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
                                                                                                                                                                          ch 100.0%; Score 101; DB 23; Length 238; l Similarity 100.0%; Pred. No. 9e-08; 17; Conservative 0; Mismatches 0; Indels 0
50 WIDPENGDSDYAPKFOG 66
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1: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_Dep:*
/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB_Dep:*
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US-09-865-198-28
1 US-09-788-689-21
1 US-09-798-689-2
1 US-09-788-689-2
1 US-09-976-787-2
1 US-09-865-198-2
1 US-09-865-198-2
1 US-10-032-482-7
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Sequence 22, Appl
Sequence 21, Appl
Sequence 23, Appl
Sequence 22, Appl
Sequence 7, Appli
Sequence 28, Appl
Sequence 28, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 2, Appli
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APPLICANT Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDF
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT APPLICATION NUMBER: US 09/493,539
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 22
LENGTH: 17
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Best Local Similarity
Matches 17; Conserv
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TYPE: PRT
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ALIGNMENTS

KDR and Uses Thereof

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RESULT 2
US-09-865-198-21
; Sequence 21, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
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                                                                                                                                                                    100.0%; ilarity 100.0%; Conservative 0;
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Pred. No. 3.4e-09;
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; ORGANISM: Mouse
US-09-865-198-21
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SEQ ID NO 23
LENGTH: 11
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APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding
TITLE OF INVENTION: Production
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Sequence 23, Application U
Patent No. US20020064528A1
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SOFTWARE: WordPerfect
SEQ ID NO 21
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                                                                     FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR KILING DATE: 2000-05-24
   SOFTWARE: WordPerfect 8.0 for Windows EQ ID NO 22
LENGTH: *117
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APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CÜRRENT APPLICATION NUMBER: US/09/976,787
CÜRRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR APPLICATION NUMBER: US 09/493,726
PRIOR APPLICATION NUMBER: US 09/493,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
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                                                        NUMBER OF SEQ ID NOS:
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CÜRRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
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Pred. No. 2.5e-08;
; Mismatches 0;
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SEQ ID NO 29
LENGTH: 238
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TYPE: PRT
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1996-0
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                                      SOFTWARE:
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ORGANISM: Mouse
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DR FILING DATE: 1995-08
DR APPLICATION NUMBER:
DR FILING DATE: 1994-11
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APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
            PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
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WordPerfect 8.0 for Windows
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100.0%; Pred. No.
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; ORGANISM: Mouse
US-09-865-198-28
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FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
SOFTWARE: WordPerfect 8.0 for Windows
SOCTWARE: WordPerfect 8.0 for Windows
LENGTH: 238
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Patent No.
                                                                                                                                                                               APPLICANT: Goldstein, Neil I.
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined with Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/901,163
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 08/567,113
PRIOR APPLICATION NUMBER: 08/67,13
PRIOR APPLICATION NUMBER: 08/706,804
PRIOR APPLICATION NUMBER: 08/706,804
PRIOR PILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/476,533
PRIOR PRIOR APPLICATION NUMBER: 08/476,533
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                 SOFTWARE:
SEQ ID NO 21
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Publication No. US2003010197777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                     PRIOR APPLICATION PRIOR FILING DATE:
                                                                    NUMBER OF SEQ ID NOS:
ENGTH: 238
                                                                                       APPLICATION NUMBER: 08/
FILING DATE: 1994-02-10
                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28, Application US/09865198
0. US20020103345A1
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                                           PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rockwell, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhenping
                                                                                                                                      1994-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 101; DB 10; 100.0%; Pred. No. 5.2e-08; ative 0; Mismatches 0;
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Pred. No. 5.2e-08;
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APPLICANT: Goldstein, Neil I.

APPLICANT: Goldstein, Neil I.

ITITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists

ITITLE OF INVENTION: Combined With Radiation and Chemotherapy

FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP

CURRENT APPLICATION NUMBER: US/09/798,689

CURRENT FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 09/401,163

PRIOR APPLICATION NUMBER: 09/401,163

PRIOR FILING DATE: 1999-09-23

PRIOR PRIOR APPLICATION NUMBER: 08/706,804

PRIOR PRIOR DATE: 1995-00-03

PRIOR APPLICATION NUMBER: 08/706,804

PRIOR APPLICATION NUMBER: 08/476,533

PRIOR APPLICATION NUMBER: 08/326,552

PRIOR APPLICATION NUMBER: 08/326,552

PRIOR PILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 08/326,552

PRIOR FILING DATE: 1995-01-020
                                                                                              APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
APPLICANT: Witte, Larry
APPLICANT: Witte, Larry
APPLICANTON: Antibodies Specific to KD:
FILE REFERENCE: 11245/46505
CCURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1909-01-29
NUMBER OF SEQ ID NOS: 40
NUMBER OF SEQ ID NOS: 40
NUMBER OF SEQ ID NOS: 40
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Publication No. US20030103973A1
GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09976787 Patent No. US20020064528A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
SEQ ID NO 2
LENGTH: 16
                  SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 2
LENGTH: 17
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Mus musculus
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100.0%; Pred. No.
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Pred. No. 5.2e-08;
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2.7e-08;
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; ORGANISM: Mus musculus US-10-032-482-18
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; ORGANISM: Mouse
US-09-865-198-2
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                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/032,482
CURRENT FILING DATE: 2002-01-02
PRIOR APPLICATION NUMBER: US/09/445,602
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: PCT/IL98/00266
PRIOR APPLICATION NUMBER: PCT/IL98/00266
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: IL 121041
PRIOR FILING DATE: 1997-06-09
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                                                                                                                          SOFTWARE: POSEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/10032482 Publication No. US20020197270A1
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SEQ ID NO 2
LENGTH: 17
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and MethorITITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                             APPLICANT: RUIZ, Pedro
APPLICANT: ERRZ-ALON, Neta
APPLICANT: HERKEL, Johannes
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
TITLE OF INVENTION: IMMUNITY
                                                                                                                                                                NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cohen,
APPLICANT: ROTTE
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PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
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                                                                                        TYPE: CPRT
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Local Similarity 94.1%;
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                                                                                                                                             PatentIn version 3.0
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94.1%;
93.1%;
88.2%;
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Score 94;
Pred. No.
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Pred. No. 4
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Pred. No. 4.2e-08
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DB 14;
4.2e-08;
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               Length 17;
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US-09-976-787-7
                                                                                          US-09-976-787-7
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US-10-032-482-7
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APPLICANT: Cohen, II
APPLICANT: ROTTER,
APPLICANT: Wolkowic
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     Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                              SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09976787 Patent No. US20020064528A1
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PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                               NUMBER OF SEQ ID NOS: 40 SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
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                                                                                                  TYPE: PRT ORGANISM: Mus musculus
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                                                                                                                                           JENGTH: 117
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Local Similarity 88.2%;
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HERKEL, Johannes
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                Conservative
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                                93.1%;
94.1%;
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                  Mismatches
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GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
ITITLE OF INVENTION: Antibodies Specific to
FILE REFERENCE: 11245/46505
CURRENT APPLICATION UNDERS: US/09/976,787
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: IMMUNITY

TITLE OF INVENTION: IMMUNITY

FILE REFERENCE: COHEN42

CURRENT APPLICATION UNMEER: US/10/032,482

CURRENT FILING DATE: 2002-01-02

PRIOR APPLICATION UNMEER: US/09/445,602

PRIOR APPLICATION UNMEER: US/09/445,602

PRIOR PILING DATE: 2001-01-24

PRIOR APPLICATION UNMEER: PCT/1L98/00266

PRIOR APPLICATION UNMEER: IS/09/445,602

PRIOR APPLICATION UNMEER: DCT/1L98/00266

PRIOR APPLICATION UNMEER: IS/09/1198/00266

PRIOR APPLICATION UNMEER: IS/09/1198/00266

PRIOR APPLICATION UNMEER: IS/09/1198/00266
Score 94; DB 9
Pred. No. 3e-07
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Pred. No.
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Indels

Gaps

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Sequence 7, Application US/09865198

Patent No. US20020103345A1

GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102

CURRENT APPLICATION NUMBER: US/09/865,198

CURRENT APPLICATION NUMBER: US/09/865,198

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 60/206,749

PRIOR FILING DATE: 2000-05-24

NUMBER OF SEQ ID NO5: 34

SOPTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 7

LENGTH: 117

TYPE: PRT

ORGANISM: Mouse

US-09-865-198-7
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Search completed: July 30, 2003, 10:20:29 Job time : 20.897 secs
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US-09-865-198-7
                                                                                                                                                                             Query Match 93.1%; Score 94; DB 10; Length 117; Best Local Similarity 94.1%; Pred. No. 3e-07; Matches 16; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                             0; Gaps
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                 Score
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gn2-6/ptodata/1/paa/US089_COMB.pep:*
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gn2-6/ptodata/1/paa/US097A_COMB.pep:*
gn2-6/ptodata/1/paa/US097B_COMB.pep:*
gn2-6/ptodata/1/paa/US097B_COMB.pep:*
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PCT-US02-41372-21
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Sequence 21, Appl
Sequence 21, Appl
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ALIGNMENTS

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APPLICANT: Zhu, Zhenping
ITITLE OF INVENTION: Bispecific Antibodies That Bind to
FILE REFERENCE: 11245/48576
CURRENT APPLICATION NUMBER: PCT/US02/20332
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: US 60/301,299
PRIOR FILING DATE: 2002-06-26
INUMBER OF SEQ ID NOS: 137
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 21
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
PCT-US02-20332-21
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                                                                                                                                     ; ORGANISM: Mouse PCT-US02-20332-21
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                                                            Matches
                                                                          Query Match
Best Local
                                                                                                                                                                          TYPE: PRT
                                                          17;
1 WIDPENGDSDYAPKFQG
                                                          h 100.0%; Score 101; DB 1; Similarity 100.0%; Pred. No. 1.1e-08; 17; Conservative 0; Mismatches 0;
                                                                                              Length 17;
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PCT-US02-41372-21
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US-09-539-692-2
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LENGTH: 17
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APPLICANT: Witte, Larry
APPLICANT: Rafii, Shahin
TITLE OF INVENTION: Treatment of Non-Solid Mammalian Tumors with Vascular Endothelial
TITLE OF INVENTION: Growth Factor Receptor Antagonists
FILE REFERENCE: 11245/46701
CURRENT APPLICATION NUMBER: US/09/540,770
CURRENT FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kerbel, Robert
TITLE OF INVENTION: Therapeutic Method for Reducing Angiogenesis
FILE REFERENCE: Sequence Listings 1-16 for 11245-19
CÜRRENT APPLICATION NUMBER: US/09/539,692
CÜRRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/178791
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 11245/485762
CURRENT APPLICATION NUMBER: PCT/US02/41372
CURRENT FILING DATE: 2002-12-24
PRIOR APPLICATION NUMBER: PCT/US02/20332
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/301,299 PRIOR FILING DATE: 2002-06-26
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TITLE OF INVENTION: Bispecific Antibodies That Bind to VEGF Receptors
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Pred. No. :
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Pred. No. 1.1e-08;
Mismatches 0;
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         RESULT 7
US-09-976-787-22
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; ORGANISM: Mouse
US-09-865-198-21
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; ORGANISM: Mouse
US-09-559-019-21
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SEQ ID NO 21
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                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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ORGANISM: Mouse
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NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 21
LENGTH: 17
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APPLICANT: Zhu, Zhenping
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LENGTH: 17
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APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
                                                                                                                                                                                                                            TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR PILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: Sequence Listings 1-34 for CURRENT APPLICATION NUMBER: US/09/559,019 CURRENT FILING DATE: 2000-04-25 NUMBER OF SEQ ID NOS: 34
1 WIDPENGDSDYAPKFOG 17
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                                                   Score 101; DB 23;
Pred. No. 1.1e-08;
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Pred. No. 1.1e-08;
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Application US/09976787

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APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Antibodies That Bir
TITLE OF INVENTION: Bispecific Antibodies That Bir
TITLE REFERENCE: 11245/48576
CURRENT APPLICATION NUMBER: PCT/US02/20332
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: US 60/301,299
PRIOR PILING DATE: 2002-66-26
NUMBER OF SEQ ID NOS: 137
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 22
LENGTH: 117
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PCT-US02-20332-22
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                                                                                                                                                                      Sequence 22, Application PC/TUS0241372
GENERAL INFORMATION:
APPLICANT: 2hu, Zhenping
TITLE OF INVENTION: Bispecific Antibodies That Bind
FILE REFERENCE: 11245/485762
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Best Local Similarity
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Best Local (
                                                    CURRENT APPLICATION NUMBER: PCT/US02/41372
CURRENT FILING DATE: 2002-12-24
PRIOR APPLICATION NUMBER: PCT/US02/20332
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/301,299
PRIOR FILING DATE: 2002-06-26
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 137
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 22
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NUMBER OF SEQ ID NOS: 40
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Witte, Larry
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Best Local Similarity
Matches 17; Conserva
                                                                                                                              ; ORGANISM: Mouse US-09-540-770-7
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US-09-540-770-7
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LENGTH: 117
TYPE: PRT
ORGANISM: Mouse
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SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 7
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                                                               Matches
                                                                                               Query Match
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                                                                                                                                                                                                                                          TITLE OF INVENTION: Treatment of Non-Solid Mammalian Tumors with Vascular Endothelial TITLE OF INVENTION: Growth Factor Receptor Antagonists FILE REFERENCE: 11245/46701 CURRENT APPLICATION NUMBER: US/09/540,770 CURRENT FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Therapeutic Method for Reducing Angiogenesis FILE REFERENCE: Sequence Listings 1-16 for 11245-19 CURRENT APPLICATION NUMBER: US/09/539,692 CURRENT FILING DATE: 2000-03-31 EARLIER APPLICATION NUMBER: US 60/178791 NUMBER OF SEQ ID NOS: 16
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TYPE: PRT
ORGANISM: Mouse
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                    1 WIDPENGDSDYAPKFQG 17
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WIDPENGDSDYAPKFQG
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                                                                            Score 101; DB 19;
Pred. No. 1.1e-07;
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Pred. No. 1.1e-07;
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RESULT 12 US-09-559-019-22

Sequence 22, Application US/09559019 GENERAL INFORMATION:

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                                                                                                                                                                RESULT 14
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; ORGANISM: Mouse
US-09-559-019-22
                                                                                    Sequence 22, Application US/09865198
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
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Best Local Similarity
Matches 17; Conserv
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Best Local
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SEQ ID NO 22
LENGTH: 117
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TITLE OF INVENTION: Method for Reducing Tumor Gr
TITLE OF INVENTION: Method for Reducing Tumor Gr
TITLE OF INVENTION: Combined With Radiation and
FILE REFERENCE: Sequence Listings 1-41 for 381-
CURRENT FALLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/401,163
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
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                                    FILE REFERENCE: 11245/47102
                                                  TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 08/9
PRIOR FILING DATE: 1997-11-10
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CURRENT FILING DATE: 2000-04-25
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APPLICANT: Witte, Larry
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: Sequence Listings 1-34 for 381-71
TURRENT PAPPLICATION NUMBER: US/09/865,198
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 117
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17; Conserv
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100.0%; Pred. No. 1
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Pred. No. 1
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1.1e-07;
                                                                                                                                                                                                                                                                                                              DB 22;
1.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Search completed: July 30, 2003, 10:13:22 Job time: 95.7309 secs

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                                                                                                                             ; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23
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US-09-976-787-23
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                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: WordPerfect
SEQ ID NO 23
                                                                              Best
                                                              Matches
                                                                                            Query Match
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GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                             APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/117,726 PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/206,749 PRIOR FILING DATE: 2000-05-24
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TYPE: PRT
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                                                                                                                                                                              LENGTH: 117
                                                            Local Similarity hes 17; Conserv
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                             1 WIDPENGDSDYAPKFQG 17
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                                                              Conservative
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                                                                              100.0%; Score 101; 100.0%; Pred. No. :
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                                                              Mismatches
                                                                              1.1e-07
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                                                                                             DB 25;
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Result
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Maximum DB
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Perfect score:
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length: 2000000000
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131.295 Million cell updates/sec
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Issued Patents AA:*
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Copyright (c) 1993 - 2003
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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                 US-08-471-426-6
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US-09-672-609-3
US-09-672-609-3
US-09-672-609-7
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US-09-672-609-7
US-09-672-609-10
US-09-672-609-11
US-09-672-609-11
US-09-672-609-11
US-09-672-609-12
US-09-672-609-13
US-09-025-403A-3
US-09-025-403A-3
US-09-025-403A-7
US-09-025-403A-7
US-09-025-403A-9
US-09-025-403A-9
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US-09-025-403A-9
US-09-025-403A-9
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US-09-025-403A-9
US-09-025-403A-11
US-09-025-403A-11
US-09-025-403A-11
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ALIGNMENTS	US-09-171-945-57	US-09-171-945-19	US-09-171-945-91	US-09-171-945-89	US-09-171-945-85	US-09-171-945-81	US-09-171-945-79	US-09-171-945-75	US-09-171-945-55	US-09-171-945-11	US-09-171-945-31	US-09-102-716-16	US-09-364-088-16	US-09-188-082-16	US-08-661-052-16	US-08-983-035A-38	US-08-652-507-2	PCT-US94-01709-6
	Sequence 57, Appl	Sequence 19, Appl	Sequence 91, Appl	•	Sequence 85, Appl	Sequence 81, Appl	-	-	Sequence 55, Appl	11,	•	•	•	Sequence 16, Appl		Sequence 38, Appl	Sequence 2, Appli	Sequence 6, Appli

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US-08-017-570-4
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Patent No.
                                                                                                                                              Query Match

Best Local Similarity

Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: MEZES, PETER S
APPLICANT: KAPLAN, DONALD A
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 48641-1967
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Duane C. Ulmer STREET: P.O. Box 1967 CITY: Midland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4, Application US/08017570
o. 5472693
WIDPENGDSDYAPKFQG
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                              Conservative
                                        93.1%;
         17
                               2
                                        Score 94; DB 1;
Pred. No. 8e-08;
                               Mismatches
                                                   Length 124;
                               Indels
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                              Gaps
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WIDPENGDTEYAPKFOG

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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION UNMBER: 34,941
REFERENCE/DOCKET NUMBER: C--
TELECOMMUNICATION INFORMATION:
                                                                       NUMBER OF SEQUENCES:
                                                                                   TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
                                                                                                                  APPLICANT:
                                                                                                                                  APPLICANT:
                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                         CCRRESPONDENCE
                                                                                                                                                                             PPLICANT:
                          STREET:
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US
FILING DATE: 19930216
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
             TY: Midland
                                           DRESSEE:
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AMINO ACID
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                                                                                                                                                                                                                         Application US/08471426
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                             P.O. Box 1967
                                                                                                                               RIXON, MARK W
MEZES, PETER S
KAPLAN, DONALD A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIXON, MARK W
MEZES, PETER S
                                                                                                                  SCHLOM, JEFFREY
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                                ADDRESS:
                                         Duane
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Pred. No.
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US-08-471-426-6
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                                                                                                                                                     COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/017,570
PILING DATB: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: 08/017,570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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88.2%; Pred. No.
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                    C-38,777
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US-09-672-609-3
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Best Local Similarity
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PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Minimum 1998-02-18
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                                                                                                                               APPLICANT:
APPLICANT:
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                                           CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                         APPLICANT: Anderson, W.H. Ker APPLICANT: Tempest, Philip R.
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APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized
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NUMBER OF SEQ ID NOS:
SOFTWARE: Microsoft
EQ ID NO 3
                                                                                                               APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized
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                                                                                                    FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: Murine Col-1 VH
LOCATION: 1..124
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               Microsoft Word 97 SR-2
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Pred. No.
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Pred. No.
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8e-08;
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                                                                                                                  Anti-CEA Monoclonal Antibodies
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RESULT 7
US-09-672-609-4
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US-09-672-609-5
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Best Local S
Matches 15
                                                                                                           GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
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SEQ ID NO 4
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                                                                                                                                                              Sequence 5, Application US/09672609 Patent No. 6333405
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Best Local Similarity
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
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APPLICANT:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
                               TITLE OF INVENTION:
FILE REFERENCE:
                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: NAME/KEY: Humanized COL-1 VH, HuVHA LOCATION: 1..124
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LOCATION: 1..124
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TYPE: PRT
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Microsoft Word 97 SR-2
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Tempest, Philip R.
Carr, Frank J.
Harris, William J.
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WIDPENGDTEYAPKFQG 66
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                                                                             Carr, Frank J.
Harris, William J.
                                                                 Armour,
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High Affinity Humanized
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Pred. No. 8e-0
2; Mismatches
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Pred. No. 8e-08;
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                                                  Anti-CEA Monoclonal Antibodies
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RESULT 10
US-09-672-609-7
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US-09-672-609-6
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SOFTWARE: Micr
; SEQ ID NO 5
FNGTH: 124
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Best Local S
Matches 15
                                                            Sequence 7, Application US/09672609
Patent No. 6333405
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
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Patent
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SEQ ID NO 6
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PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
APPLICANT:
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APPLICANT: Harris, William J.
APPLICANT: Armour, Wailliam J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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OTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, OTHER INFORMATION: Ile-29, Lys-30, Ala-79, Asn-97, and Thr-98
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OTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
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Similarity 88.2%;
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                              Anderson, W.H. Kerr
Tempest, Philip R.
Carr, Frank J.
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Tempest, Philip R.
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Pred. No. 8e-08;
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Pred. No. 8e-08;
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SEQ ID NO 7
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CURRENT FILING DATE: "2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
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TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
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                                                                                                                                                         OTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala 24, Phe-27, Asn OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn; 97, and Thr-98
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NAME/KEY: Humanized COL-1 VH, HUVHATAY
LOCATION: 1..124
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHAY
LOCATION: 1..124
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Tempest, Philip R.
Carr, Frank J.
Harris, William J.
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High Affinity Humanized Anti-CEA Monoclonal Antibodies
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88.2%; Pred. No. 8e-
tive 2; Mismatches
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US-09-672-609-9

Sequence 9, Application US/09672609 Patent No. 6333405

RESULT 12

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FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
FRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 10
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Patent No. 6333405
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CURRENT FILING DATE: 2000-09-28
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APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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OTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FR8, murine COL-1 VH CDRs, and Ala-24, Phe-27, OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, Tyr-80, Asn-97, OTHER INFORMATION: Thr-98
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NAME/KEY: Humanized COL-1 VH, HuVHT
                                                                                                                                          LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWN VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28, OTHER INFORMATION: Ile-29, Lys-30, Thr-72, Asn-97, and Thr-98
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ORGANISM: Artificial Sequence
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Armour, Kathryn
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Tempest, Philip R.
Carr, Frank J.
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Pred. No. 8e-08;
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Pred. No. 8e-08;
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PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 12
LENGTH: 124
TYPE: PRT
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US-09-672-609-12
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SEQ ID NO 11
LENGTH: 124
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Appli
Patent No. 6333405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Carr, Frank J. APPLICANT: Harris, William J. APPLICANT: Harris, William J. APPLICANT: Armour, Kathryn TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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FILE REFERENCE:
FEATURE: Humanized COL-1 VH, HuVHSTAY NAME/KEY: Humanized COL-1 VH, HuVHSTAY LOCATION: 1..124

OTHER INFORMATION: Humanized heavy chain CTHER INFORMATION: CRL-12208, and content of the CTHER INFORMATION: and phe-27, ken-28, CTHER INFORMATION: Tyr-80, Asn-97, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Humanized COL-1 VH, HuVHS
LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWN VH FRS, murine COL-1 VH CDRs, and Phe-27, Asn-28,
OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Asn-97, and Thr-98
                                                                                                                                                          ORGANISM: Artificial Sequence
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Local Similarity 88.2%;
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Harris, William J.
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Tempest, Philip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson, W.H. Kerr
Tempest, Philip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09672609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
  Humanized heavy chain variable region expressed from ATCC CRL-12208, and containing human NEWM VH FRs, murine COL-1 VH CDRs and Phe-27, Asn-28, Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, Tyr-80, Asn-97, and Thr-98
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Pred. No. 8e-08;
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Best Local Similarity 88.2%; Pred. No. 8e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGDSDYAPKFQG 17
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Db 50 WIDPENGDTEYAPKFQG 66

Search completed: July 30, 2003, 09:38:30

Job time: 5.4784 secs
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ALIGNMENTS

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Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C;Accession: S04576
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Tleur. J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involvemental preference number: S04576
A;Accession: S04573; MUID:87133856; PMID:3102255
A;Accession: S04576
A;Molecule type: mRNA
A;Residues: 1-136 <KOP>
A;Cross-references: EMBL:X14624; NID:952029; PIDN:CAA32777.1; PID:952030
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                       Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
(;Species: Mus musculus (house mouse)
(;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
(;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is function and the sequence number: A56446; MUID:95229583; PMID:7713873
A;Accession: A56446
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Residues: 1-268 <TAN-
A;Residues: 1-268 <TAN-
A;Residues: heterotetramer; immunoglobulin
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A56446
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Query Match
Best Local Similarity
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82.9%;
79.0%;
83.1%;
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Score 498.5; DB 2
Pred. No. 9.5e-38;
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Pred. No. 3.5e-39;
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A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
A;Accession: S33133
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <MO2>
A;Residues: 1-118 <MO2>
A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change (c;Accession: $25174; $33133
R;Monestier, M; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, submitted to the EMBL Data Library, July 1992
A;Description: Structure and binding properties of monoclonal ant A;Reference number: $25174
A;Reference number: $25174
A;Accession: 
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c;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S15672
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                                                                                              Query Match
Best Local S
Matches 93
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                                                                                              Conservative
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78.8%;
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                                                                                        Score 491; DB 2; 1
Pred. No. 1.9e-37;
0; Mismatches 13;
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М.
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Ig heavy chain V region (B8) - mouse (fragment)
c;Species: Mus musculus (house mouse)
C;Date: 22-Nov-193 #sequence_revision 26-May-1995 #text_change 21-
C;Accession: S17586
C;Accession: S17586
C;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region precursor - mouse (;Species: Mus musculus (house mouse) C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change C;Accession: S52445 R;Berdoz, J.; Kraehenbuhl, J.P.
                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain: immunoglobulin homology <
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                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary A; Molecule type: mRNA
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A; Residues: 1-137 <BER>
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A; Accession: S52445
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                                                                                                                                                                                 93;
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                                                                                                                                                                            Similarity 78.8
93; Conservative
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                  APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAY-YGDYEGYWGQGTTVTVSS 117
                                                                                                               QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                       EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEKGLEWIGRIBPASGNTKY
DPKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCAGYDYGNFD-YWGQGTTLTVSS
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78.8%;
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78.2%;
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Pred. No. 1.9e-36;
2; Mismatches 11
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Pred. No. 1.6
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A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983 A;Note: this sequence was determined from the differentiated gene R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire A;Reference number: S07453; MUID:83058021; PMID:6815271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03471
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                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 1-43 < ROC2>
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EMBO J. 2, 867-872, 1983
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C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision
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A; Residues: 7-120 < ROC1 >
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: immunoglobulin
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A;Description: Cloning and
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R;Kipp, B.; Becker,
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                                                                                                                                                                                                                                                             Superfamily: immunoglobulin V region, immunoglobulin; Keywords: heterotetramer; immunoglobulin; 15-98/Domain: immunoglobulin homology <IVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;121-221/Domain: C region #status predicted <C:;139-203/Domain: immunoglobulin homology <IMM>
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Best Local Similarity
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Best Local
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                       APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYY--GDYEGYWGQGTTVTVSS
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DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARGWLRRDAMDYWGQGTSVTVSS
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                                                                                  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY
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79.0%;
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79.0%;
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Pred. No. 4.5e-36;
6; Mismatches 17
                                                                                                                                                                                                 Score 476; DB 2;
Pred. No. 4.4e-36;
                                                                                                                                                                            Mismatches
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R;Moncharmont, B. submitted to the EMBL Data Library, September 1991 A;Description: Cloning and sequencing of the cDNA A;Reference number: $24287 A;Accession: $24289
A;Note: Mus musculus (house mouse) gene engineered C;Date: 21-Sep-1993 #sequence_revision 11-Aug-1995 C;Accession: A47271 R;Lesley, S.A.; Patten, P.A.; Schultz, P.G. Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993 A;Title: A genetic approach to the generation of ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X62705; NID:g51690; PIDN:CAA44584.1; PC:Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: immunoglobulin C;Keywords: immunoglobulin homology <IMM>
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C;Date: 20-Feb-1995
C;Accession: S24289
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S24289
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C;Species: Mus musculus (house mouse)
C;Date: 06-Uan-1955 #sequence_revision 0
C;Accession: $29594
R;Seymour, R.
submitted to the EMBL Data Library, Febr
A;Reference number: $29593
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S29594
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C;Keywords: immunoglobulin
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A; Residues: 1-116 < MON>
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A; Residues: 1-178 <SEY>
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C;Species: Mus musculus (house mouse)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                      62 PKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                              VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD
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78.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.0%; Score 467; DB 2; 76.7%; Pred. No. 2.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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Pred. No. 1.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              February 1991
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                                                                                    and expressed in Escherichia #text_change 11-Aug-1995
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                                                                                                                                                      synthetic (fragment)
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Jaion: 80,
A;Molecule type: n.
A;Residues: 1-1~
C;Superfam;
C;Keywo~
F;1"
                                                                                                                                                                p53 specific single-chain antibody Pab421 - C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-Ma
C;Accession: JC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A47271; MUID:93165660; PMID:8094556
A;Accession: A47271
A;Accession: A47271
A;Molecule type: DNA; protein
A;Residues: 1-114 <LES>
A;Note: sequence extracted from NCBI backbone (NCBIN:124854, NCBIP:124855)
A;Note: parts of this sequence were determined by protein sequencing
F;22-96/Disulfide bonds: #status predicted
                                                                                              A;Title: Characterization of scFv-421, a single-chain a A;Reference number: JC5322; MUID:97168950; PMID:9016757 A;Accession: JC5322 A;MOIecule gype: mRNA
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_c
C;Accession: $06823
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses
A;Reference number: $06815; MUID:90064531; PMID:2555519
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                              Comment: This protein
                                                                        ; Molecule type: mRNA; Residues: 1-233 < JAN>
  Query Match
                                                          Experimental source: hydricloma
                                                                                                                                                                                                                             Species: Homo sapiens (man)
Date: 15-May-1997 #sequence_revision 15-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
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pecies: Mus musculus (house mouse)
pate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARGWLRRDAMGVDYWGQGTSVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVKLLESGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRIDPANVDTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin homology < IMM>
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                                      specifically
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77.8%;
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77.9%;
                                                                                                                                                                      230, 242-246, 1997
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Pred. No. 9e-3
8; Mismatches
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Score
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Pred. No. 3.7e-35;
                                  binds the tumor suppressor protein
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459;
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Length
                                                                                                                                                      antibody targeted
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A;Molecule type: mRNA
A;Residues: 10-115 <ROC1>
A;Cross-references: EMBL:X03219
A;Note: this sequence was determined from
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: S07453; MUID:83058021; PMID:6815271 A;Accession: S07453
                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
A;Varriety: strain BALB/C
C;Date: 26-Feb-198 #sequence_revision 26-Feb-1998 #text_change 21 Jan-2000
C;Accession: S03482; S07453
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A; Residues: 1-43 < ROC2>
C; Superfamily: immunoglob
F; 15-98/Domain: immunoglo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: this sequence was determined from R; ROCCa-Serra, J.; Mazie, J.C.; Moinier, E J. Immunol. 129, 2554-2558, 1982
A; Title: The limited diversity of the mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 10-120 <ROC1>
A;Cross-references: EMBL:X07144
                                                                                                                 A; Reference number: S03471;
A; Accession: S03482
                                                                                                                                                                           EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
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                                                                                               A;Status: preliminary
                                                                                                                                                         hypervariable regions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus
A;Variety: strain BALB/c
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Best Local
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-98/Domain: immunoglobulin homology
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QY 61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTV 115 : :
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Query Match Best Local & Matches 88
Status: preliminary Molecule type: protein Molecule type: protein Residues: 1-43 <roc2> Recidues: 1-43 <roc2> Residues: 1-43 <roc2> Superfamily: immunoglobulin V region; immunoglobulin homology 15-98/Domain: immunoglobulin homology <imm> 71.9%; Score 454; DB 2; Length 115; Best Local Similarity 76.5%; Pred. No. 4e-34; Best Local Similarity 76.5%; Pred. No. 4e-34; Best Local Similarity 76.5%; Pred. No. 4e-34; 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60 </imm></roc2></roc2></roc2>

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-i- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED
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Mus musculus (Mouse).

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120 AA;
         (Rel. 01, Created)
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ain V region S43 precursor.
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62.5%;
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Pred. No. 6.2e-32;
9; Mismatches 22;
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Pred. No. 3.4e-33;
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Best Local :
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InterPro; IFAC.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
SMART; SM0040635; IG LIKE; 1.
TOCTTE; PS50835; IG LIKE; 1.
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HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
TherPro; IPR003006; Ig_MHC.
TherPro; Trann3596; Ig_v.
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus MCBI_TaxID=10090;
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SEQUENCE FROM N.A.
                                                      Mus musculus (Mouse)
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Cell 24:625-637(1981)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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L.M., Paskind M., Reth
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IES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)AÇETYL
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BY SIMILARITY.
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D SEGMENT.
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COMPLEMENTARITY-DETERMINING-2.
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Matches 74
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InterPro; IPKuussi
Pfam; pF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
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21-JUL-1986
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SEQUENCE
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as a modified and this statement is not removed. Us
"Complete amino acid sequence of a mouse mu chain: heavy chain constant region domains."; Biochemistry 21:5415-5424(1982).
-i- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN PROTEIN HAS ALSO BEEN DETERMINED.
-i- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                              NCBI_TaxID=10090;
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Mammalia; Eutheria;
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Science 216:309-311(1982).
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MEDLINE=82152818;
                                                                                 MEDLINE=83075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Capra J.D.;
                                                                                                            SEQUENCE,
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(Rel. 01, Last sequence update)
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avy chain.";
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15514 MW;
                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 381; DB 1;
Pred. No. 5.7e-31;
2; Mismatches 20
                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25A4CBBE31DA5CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEAVY CHAIN V REGION 93G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variable portion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Slaughter C.,
                                                                                   J.W.,
                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions ng as its content is in
                                                                                                           ASN-55
                                                                                                                                                                                                                                              B
                                                                                 Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                          읶
                                                           homology
                                                                                                                                             Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ķ
                                                                                   Sibley C.H.,
                          THIS IGM MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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RESULT
HV48_M
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Best Local S
Matches 73
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; 19,

SMART; SM00406; IGv; 1.

SMART; SM00406; IG LIKE; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Glycoprotein.

Immunoglobulin V region; Glycoprotein.

BY SIMILARITY

96

"TTNKED (GLC
                                                                                                                                                                                                                                                                                                                                                                                                                                      HV48 MOUSE
P03980;
23-OCT-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID CARBOHYD NON_TER
                                            DISULFID NON_TER
                                                                          DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 immunoglobulin-like domain PIR; A02039; MHMS4E.
HSSP; P01789; IMCP.
                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                  delta in an IgD-secreting plasmacytoma."
Proc. Natl. Acad. Sci. U.S.A. 81:4164-41
                                                                                                                                                                                                                                                                                                             Gilliam A.
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                        SMART; SM00406;
                                                                                                                                                                                                                                                                                                     Tucker P.W.;.
                                                                                                                                                                                                                                                                                                            MEDLINE=84248078; PubMed=6429663; Gilliam A.C., Shen A., Richards J.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1986
                                                                  DOMAIN
                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                 Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [nterPro;
                                                                                                                                                                  mmunoglobulin
                                                                                                                                                                                                                                               ISSP; P01810;
                                                                                                                                                                                                                                                                                        Illegitimate recombination generates a class
                                                                                                                                                                                                                                                                                                                                                                                                                  5-JUL-1999
                                                                                                                                                                                                                                                        A02033; HVMST7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                           M00406; IGv; 1.
PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDYDWYFDVWGAGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVOLOGSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                    ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 02, Last sequence update)
(Rel. 38, Last annotation update)
ain V region TEPC 1017 precursor.
                                 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                           21
50
55
69
86
118
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                  region;
                                                                                                                                                                                                                                                                                                                                                                                                                 02,
38,
                                                                 49
68
68
117
117
138
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                                 15576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.7%;
59.3%;
61.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                 Signal
                                 Œ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 377; DB Pred. No. 1.2e
Score 374; DB 1;
Pred. No. 2.8e-30;
                                                     FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                     IG HEAVY CHAIN V REGION TEPC 1 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC.
                                                                                               FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                     81:4164-4168(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3CF8ACE4BE447E41 CRC64;
                                 748157E4C6907B8E
                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             138
                                                                                                                                                                                                                                                                                                              Blattner F.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2e-30;
                                                                                                                                            REGION TEPC 1017.
                                                                                                                                                                                                                                                                                          switch
                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
          Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .) (COMPLEX).
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                                                                                                                                                                                                                                                                                        from
                                                                                                                                                                                                                                                                                                              Mushinski J.F.,
                                                                                                                                                                                                                                                                                                                                                                       Murinae; Mus
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Strober S.,

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RESULT 8
HV15_MOUSE
ID HV15 M
AC P01759
DT 21-JUL
DT 21-SEP
DE IG hear
OS Mus mus
OC Eukary
OC Mammal
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HV13_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CerPro; it.
LterPro; IPR0035...
LterPro; IPR0035...
LterPro; IPR0035...
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
I 116
I 116
I 12 96
I 17
I 17024 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P01789; 1MCP.
InterPro; IPR007110; 1
InterPro; IPR003006; 1
InterPro; IPR003596; 1
                                                  HV15 MOUSE STANDARD; PRT; 136 AA. P01759; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP;2003 (Rel. 42, Last annotation update) 19 heavy chain V region BCL1 precursor.
                      Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=80078170; PubMed=6765983; Schilling J., Clevinger B., Davie J.M., Hood L.; Schilling J., Clevinger B., Davie J.M., Hood L.; "Amino acid sequence of homogeneous antibodies to dextran rearrangements in heavy chain V-region gene segments."; Nature 283:35-40(1980).

-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A26242; MHMSJ5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01757;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         !- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHICH OCCUR IN THE D AND J SEGMENTS MISCELLANEOUS: THIS PROTEIN BINDS D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
73; Conserv
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                                                                                                                                                                                                                                                                                          NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRYW--YFDVWGAGTTVTVSS
                                                                                                                                                                                                                                                                                                                                   APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGDYEGYWGQGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                            QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEXTRAN DIFFER FROM THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC---NAYYGDYEGYMGQGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY
      Butheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01, Last sequence update)
42, Last annotation update)
                      Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig-like.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 368; DB 1; 1
Pred. No. 9.1e-30;
6; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE.
BY SIMILARITY.
                         Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; |
Sciurognathi; Muridae;
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292E2AF4BE447E41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NMOHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEXTRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N AT 1-7 PO
                         Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
  Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POSITIONS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
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OF
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HV50_MC
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Best Local S
Matches 69
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lymphocytes is encoded by a
EMBO J. 3:517-523(1984).
PIR; A02037; MHMS15.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988
01-JAN-1988
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                         HV50 MOUSE
P06329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin signal 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by a cloned B-cell lymphoma: a single copy by two adjacent CH genes.";

Proc. Natl. Acad ori
                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=82222262; PubMed=6806821;
MEDLINE=82222262; PubMed=1806821;
                                                                                                                                                                          Dildrop R., Bovens
                                                                                                                                                                                          SEQUENCE:
MEDLINE=84182519; PubMed=6201362;
                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                       ig heavy chain
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SM00406; IG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOKFKGKATMTVDKSSSTVHMELARLTSEDSANLYCARYYGNYFDYWGQGTTLTVSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYNGNTSY 79
                      IPR007110;
IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136
136 /
                                                                                                                                                                                                                                                                                                                                                     (Rel. 06, Created)
(Rel. 06, Last sequence up
(Rel. 38, Last annotation
ain V region AC38 15.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sci. U.S.A. 79:2996-3000(1982)
                                                                                                                               J., Siekevitz M.,
inant (idiotope) es
oded by a large se
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Ig-like.
Ig_MHC.
Ig_v.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 368; L.
No. 1:1e-29;
3)
                                                                                                                                 M., Beyreuther K., Rajewsky K.;
expressed at high frequency i
set of antibody structural gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ward R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGION
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the
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VH gene is shared
                                                                                                                                                                                                                                                                                       Murinae; Mus.
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Gaps

60 0

genes.";

Pfam; PF00047; SMART; SM00406;

ig; igv; iGv;

LIKE;

PROSITE;

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PFFFFKRRRDDRREDRRETTFFFKRRRDDRRETTFFFFFFFF
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HV1C_HUMAN
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Best Local S
Matches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin '
DOMAIN 1
DOMAIN 99
DOMAIN 106
                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986
16-OCT-2001
15-SEP-2003
DOMAIN
MOD RES
DISULFID
                                                                                                                               HSSP;
GO; GC
GO; GC
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NON TER
SEQUENCE
                                       Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE;

Immunoglobulin V region; S:

SIGNAL 1 19
                                                                                                                                                                                         SEQUENCE OF 20-147.

Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;

(In) Bach M.K. (eds.);

Immediate hypersensitivity: modern concepts and develo;

Marcel Dekker, New York (1978).

-i- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FRO
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=83065234; PubMed=6815656;

Kenten J.H., Molgaard H.V., Houghton M., Derbyshire

Mell L.O., Gould H.J.;

"Cloning and sequence determination of the gene for

immunoglobulin epsilon chain expressed in a myeloma

Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence upon 15-SEP-2003 (Rel. 42, Last annotation upon 15 heavy chain V-I region ND precursor
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                              P; P01789; 1MCP.
GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding act
GO:0006955; P:immune response; NP
                                                                                                                                                                        SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEG-----YWGQGTTVTV
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106
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13311 MW;
147
131
20
115
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Primates;
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105
120
96
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                                                    Signal; Pyrrolidone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 366.5; DB 1
Pred. No. 1.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8404
          IG HEAVY CHAIN V-I REGION ND IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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) SEGMENT.
! SEGMENT.
!Y SIMILARITY.
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                                                                                                                                       activity; NAS
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ion update)
rsor (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
                                                   carboxylic acid
                                                                                                                                                                         domain
                                                                                                                                                                                                                 developments,
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                                                                                                                                                                                                                                                                                                                  R.B.,
                                                                                                                                                                                                                                                                                              human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120;
                                                                                                                                                                                                                                                                                    line.";
                                                                                                                                                                                                                                                                                                                   Viney
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RESULT

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                                                                                                                                                       Query Match
Best Local S
Matches 71
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Best Local S
Matches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Cre
01-JAN-1988 (Rel. 06, Las
15-JUL-1999 (Rel. 38, Las
Ig heavy chain V region A
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
CONFLICT
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dildrop R., Bovens J., Siekevitz M
"A V region determinant (Idiotope)
lymphocytes is encoded by a large
EMBO J. 3:517-523(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HV51_MO
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                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A02040; MHMS38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01789; 1MCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=84182519;
                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro;
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61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                           Similarity
                                  APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGY--WGQGTTVTVSS
                                                                           EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNFDYSYTLDVWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC---NAYYGDYEGY-----WGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
  NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCARGYG-YDPFDVWGTGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GITVIVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                              IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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105
                                                                                                                                                         Conservative
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06, Last sequence update)
38, Last annotation updat
region AC38 205.12.
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104
118
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                                                                                                                                                                       57.4%;
                                                                                                                                                                                                                                    12934 MW;
                                                                                                                                                                                                                                                                           96
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51.6%;
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                                                                                                                                                                                                                                                                       V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 364.5;
Pred. No. 2.6e
25; Mismatches
                                                                                                                                                     Score 362.5; DB 1
Pred. No. 3.2e-29;
7; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '-> V (IN REF. 2).
H -> HI (IN REF. 2).
G -> GV (IN REF. 2).
ISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        948F9F72A5366C20 CRC64;
                                                                                                                                                                                                                                    94F7BEE4C762A018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Beyreuther K., Rajewsky K.; expressed at high frequency in B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of.
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                                                                                                                                                                                            DB 1;
                                                                                                                                                       28;
                                                                                                                                                                                                                                    CRC64;
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                                                                                                                                                                                            Length
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                                                                                                                                                     Gaps
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                                    117
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RESULT 13
HV06_MOUSE
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SEQUENCE
                                                                                                                                                                                                                                                                                             HV06_MOUSE
P01750;
                                                           SEQUENCE FROM N.A. STRAIN=C57BL/6;
                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                             21-JUL-1986
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                 Bothwell A.L.M.,
                                   MEDLINE=81234548; PubMed=6788376;
                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                           21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zakut R., Cohen J.,
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=81053741; PubMed=6253904; Zakut R., Cohen J., Givol D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A93708; GVMS11.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR007110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                         heavy chain V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
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                                                                                                                                                                                                                                                                                                                                                                                                                            121
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; SM00406; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACIDS Res. 8:4839-4840(1980).
ELLANEOUS: THIS SEQUENCE WAS THE SECRETES IGG2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 co.
                                                                                                                                                                                                                                                                                                                                                                                                                            S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCARGIYYNSSPYFDSWGQGTTLTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APKFOGKATMTADSSSNTAYLOLSSLTSEDTAVYYC--NAYYGD--YEGYWGQGTTVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAQLQQSGAELVRPGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IPR007110; Ig-like.
; IPR003006; Ig_MHC.
; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cohen J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AA;
                                                                                                                                                                                                                               (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                       (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V region MPC 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD,
                 Paskind M.,
                                                                                                                                                                                                     01, Last sequence update)
38, Last annotation update)
region 102 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13135 MW;
                                                                                                                                                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Givol D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.2%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /KISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 348; DB 1
Pred. No. 9e-28;
                 Reth M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE
                                                                                                                                       Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227AEF3EC56ED0BF CRC64;
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                 Imanishi-Kari
                                                                                                                                                             Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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                                                                                                                                            Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
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; Murinae; Mus.
                                                                                                                                            Murinae;
                 Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRNA ISOLATED
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                                                                                                                                            Mus
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RESULT 14
HV09_MOUSE
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Best Local S
Matches 64
Immunoglobulin V
SIGNAL 1
CHAIN 20
DOMAIN 20
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    MOUSE
                    SMART; SM00406; IGv; I.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL 1
                                                   Pfam; PF00047; ig;
SMART; SM00406; IGV
                                                                                                                RELATED GENES THAT COULD PIR; D90809; HVMS61.
                                                                                                                                                "Heavy chain variable region antibodies: somatic mutation Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                     01-JUL-1989 (Rel. 11, Last sequence upda
15-JUL-1999 (Rel. 38, Last annotation up
Ig heavy chain V region 186-1 precursor.
                                                                                                                                                                                                                                                                                                                 P01753; P11271;
21-JUL-1986 (Re
                                                                                                                                                                                                                                                                                                                                        HV09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                       -!- MISCELLANEOUS:
                                                                                                                                                                                         MEDLINE=81234548;
Bothwell A.L.M., E
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin
SIGNAL 1
                                                                                                         HSSP; P01810;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 1. Immunoglobulin V region; Sign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02032; HVMS02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibodies: somatic r
Cell 24:625-637(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Heavy chain variable region contribution to the NPb family antibodies: somatic mutation evident in a gamma 2a variable
                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: THIS GERMLINE GENE BELONGS RELATED GENES THAT COULD ENCODE V REGIONS
                                                                                                                                                                                                                                                                                                                                         _NOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       PKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC
                                                                                                                                                                                                                                                                                                                                                                                            QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                     VQLQQPGAELVKPGASVKVSCKASGYTFTSYWMHWVKQRPGQGLEWIGRIHP
                                                                                                                                                                                                                                                       Eutheria;
                                                                                             IPR007110;
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                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                         paskind M., Reth
                                                                                                                            THIS GERMLINE GENE THAT COULD ENCODE V
                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Musidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.7%;
                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION 102.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
                                                                                                                                                                                          Reth
 IG HEAVY CHAIN V FRAMEWORK-1.
                                                                                                                                                          contribution to the evident in a gamma 2
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Pred. No. 1
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                                                                                                                                                                                          Imanishi-Kari T.,
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.7e-27;
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            REGION 186-1.
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                                                                                                                           A SET OF CLOSELY
                                                                                                                                                                     NPb family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT 15
HV04_MOUSI
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Matches 64
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Matches 64; Conserv
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MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
PROSITE; PS50835; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01748;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                      PIR; A02030; HVMS23.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                   antibodies: somatic n
Cell 24:625-637(1981)
                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                            -i- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                      Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                              [nterPro;
                                                                                                                                                                                                                                                                                                           nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lg heavy chain V region 23 precursor.
                                                                                                                                                                                                                                                                                    nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CBI_TaxID=10090;
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61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                    64;
                                                                                Similarity
                                                                                                                                                                                                                                   PS50835; IG LIKE; 1.
obulin V region; Signal.
                    QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPGNGGTNY
                                           QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                                                                                                                                                                                                              IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                    Conservative
                                                                                                                                                      865500
                                                                                                                  ΑĄ;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12890 MW;
                                                                             53.7%;
                                                                                                                  12772 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.4%;
                                                                 ; Score 339; DB 1;
; Pred. No. 6.8e-27;
11; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 343; DB 1;
Pred. No. 2.7e-27;
3; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
                                                                                                                                        COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
BY SIMILARITY.
                                                                                                                                                                           IG HEAVY CHAIN V REGION 23.

FRAMEWOOK.-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                        Length 117;
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                                                                    Indels
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80 NEKFKSKVTLTVDKSSSTAYTQLSSLTSEDSAVYYC 115

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Search completed: July 30, 2003, 09:45:10 Job time: 19.2691 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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Match
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631
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SPTREMBL_23:*
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Q9JL85
Q924P9
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Q924R0
Q924R2
Q924Q1
Q924R4
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Q924Q7
Q924Q3
Q921C4
Q971C5
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	Q925S2	Q9JL75	Q925S3	Q924Q0	Q8K0Z4	Q8R3H6	Q8VDC9	Q924Q8	Q9QXE9	Q8VCX7	Q921K1	Q8VCX4	Q9QXF0	Q8K0F2	Q91VA2	Q924R5	Q924R3	Q924P7	Q924Q4	Q91WT1	Q924P8	Q924R7	Q924P6	Q924Q6	Q924R6	Q924P5	Q924Q9	Q91V67	Q924Q2
	Q925s2	Q9j175	Q925s3	Q924q0	Q8k0z4	Q8r3h6	Q8vdc9	Q924q8	Q9qxe9	Q8vcx7	Q921k1	Q8vcx4	Q9qxf0	Q8k0f2	Q91va2		. Q924r3	Q924p7	Q924q4	Q91wt1	Q924p8	Q924r7	Q924p6	Q924q6	Q924r6	Q924p5	Q924q9	Q91v67	Q924q2
	mus	mus	mus	mus	Bnm	Bum	mus	mus	mus	mus	Bum	Brum	mus	mus	mus	mus	Bum	mus	mus	mus	mus	Bru	mus	mus	mus	mus	mus	Bnw	mus
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ALIGNMENTS

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RESULT 1
Q99L3
ID Q99L
AC Q99L
DT 01-J
DT 01-J
DT 01-M
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OS Mus
OC Euka
OC MCBI
RN (1)
RN (1)
RN (1)
RN SEQU
RA Stra
RL Submi
DR HSSE
DR Inte
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SQ SEQU
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                                                                                                                           Query Match
Best Local S
Matches 96
                                                                                                                                                                                    InterPro; IPRO07110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00299; IG_MHC; 1.
SEQUENCE 468 AA; 51661 MW;
                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q99L31 PRELIMINARY; PRT; 468 AA.
Q99L31; O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to GIKEN GDNA 1810060009 gene.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                               61
                                                             20
                                                                                 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDDENGDSDY
                                                                                                                           h 80.8%;
Similarity 80.7%;
96; Conservative 9
                APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGDYEGYMGQGTTVTVSS 117
                                                             APKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCARNLLYGGYYDYWGQGTTITVSS
                                                                                                                           Score 510; DB Pred. No. 2.2e-
9; Mismatches
                                                                                                                             9;
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                                                                                                                                         DB 11;
2.2e-43;
                                                                                                                             12;
                                                                                                                                                         Length 468;
                                                                                                                             Indels
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musculu

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RESULT
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Best Local
  Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometr Affinity Maturation of B Cell Antigen Receptors in Respot Hydroxy-3-Nitrophenyllheetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB069916; BAB63932.1; -.
interPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SEQUENCE
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01-DEC-2001 (TrEMBLrel. 19, Last
01-MAR-2003 (TrEMBLrel. 23, Last
V303-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                               V303-D-J-C MU.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                STRAIN=C57BL/6;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant
streptococcal polysaccharide, N-acetyl-glucosamine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JL85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M00406; IGv; 1.
PS50835; IG_LIKE;
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109 AA;
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                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
Ig-like.
Ig_MHC.
Ig_v.
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77.1%;
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Pred. No. 7
                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                          sequence up
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; Murinae; Mus
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Matches 79
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Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Affinity Maturation of B Cell Antigen Receptors in Hydroxy-3-Nitrophenyl) Acetyl (NP)."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ datal EMBL, BAB63781; BAB63266.1; InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-WHC.
InterPro; IPR003596; Ig-W.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1
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SEQUENCE 143 AA; 15704 M
Q924Q7
Q924Q7;
01-DEC-2001
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01-MAR-2003
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Mammalia; Eutheria;
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PROSITE; PS50835; IG_LIKE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by
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146 AA;
(TrEMBLrel. 19,
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ilarity 65.3%;
Conservative 1
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                                              PRELIMINARY;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 407; DB 11;
Pred. No. 1.4e-33;
4; Mismatches 24
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Pred. No. 4.9e-34;
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Sciurognathi; Muridae;
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Mismatches
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; Murinae; Mus
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RESULT
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Best Local S
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Query Match
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Matches 80
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Q924Q3;
                                                                                                                                                                                                   Kozono Y., Kozono H., Azuma T.;
Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Affinity Maturation of B Cell Antigen Receptors in Respon Hydroxy-3-Nitrophenyl) Acetyl (NP).";
Submitted (AUG-2010) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067797; BAB63282.1; -
EMBL; AB067797; BAB63282.1; -
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SEQUENCE
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Affinity Maturation of B Cell Antigen Receptors in Respondence Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. InterPro; IPR007110. Tali-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
VH186.2-D-J-C mu protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VH186.2-D-J-C mu protein
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"Direct Estimation of Relative Affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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; SM00406; IGv; 1.
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  l Similarity
80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145
145 AA;
                                                                                         146
146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145
16141 MW;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                  16136 MW; CEA8DD6E1955807F CRC64;
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                  63.9%;

    Last sequence update)
    Last annotation update)
    (Fragment).

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Pred. No. 3.2e
13; Mismatches
Score 403; DB
Pred. No. 3.7e
L4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vert
Sciurognathi;
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thi; Muridae; Murinae; Mus
DB 11;
3.7e-33;
les 23;
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                                         Length
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    Indels
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145;
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  4;
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Best Local S
Matches 78
              01-JUN-2001 (TrEMBLrel. 17, Create 01-JUN-2001 (TrEMBLrel. 17, Last si 01-MAR-2003 (TrEMBLrel. 23, Last ai Similar to RIKEN cDNA 1810060009 gMus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Cran Mammalia; Eutheria; Rodentia; Sciu NCBI TaxID=10090;
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InterPro; IPR003006; Ig_MIC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSTIE; PS50835; IG_LIKE; 1.
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Q921C4;
Q17C4;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-MAY-1999 (TrEMBLrel. 23, Last annotation update)
Anti-porcine VCAM mAb 3F4 heavy chain variable region
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SEQUENCE
                                                                                                                                                                                                    Q99L25
Q99L25;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IgG2/G4 constant regions block human
endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mueller J.P., Giannoni M.A., Hari
Matis L.M., Evans M.J.;
"Humanized porcine VCAM-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Balb/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                QVQVQQSGAELARPWASVKLSCKASGYNFNSYMMQWVKQRPGQGLEWIGAIYPGDGDTSY
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                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13036 MW;
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                                                                                                           Last sequence update)
Last annotation updat
60009 gene.
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Pred. No. 5.1e
L3; Mismatches
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                                            Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                                                update)
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                                                                 Euteleostomi;
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RESULT
QBK172
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Best Local S
Matches 78
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Best Local S
Matches 79
                                                                                                                                                                                                                                                                                   EMBL; BC028249; AAH28249.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl:
InterPro; IPR003596; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 4.
SMART; SM00407; Ig; 4.
SMART; SM00405; IGV; 1.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00835; IG_MHC; 2.
SEQUENCE 482 AA; 52121 MW; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 473 AA; 52449 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8K172;
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
similar to expressed sequence AI893585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8K172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCTR-EGDYDAMDYWGQGTSVTVSS
                         APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEG--YWGQGTTVTVSS
                                                                                                                              QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC----NAYYG----DYEGYWGQGTTV
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                                                                                          QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLQQSDAELVKPGASVKISCKVSGYTFTDHTIHWVKQRPEQGLEWIGYIYPRDGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                 63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%; Score 400.5;
63.7%; Pred. No. 2.8¢
tive 16; Mismatches
                                                                                                                                                                                             14;
                                                                                                                                                                                Score 400.5; DB 11,
Pred. No. 2.8e-32;
Wismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                        A06FF083E771D084 CRC64;
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on update)
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                                                                                                                                                                                                                                   DB 11; Length
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                                                                                                                                                                                          Indels
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RESULT 11
Q924Q5
ID Q924Q
AC Q924Q
DT 01-DE
DT 01-MA
DE VH186
CS Mus m
OC Eukar
OC Mamma
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukudai S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbish J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbish J.,
A Kuehl R., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbish J.,
A Kuehl R., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbish J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,
A Saki K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Buronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee W.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Hayashiyaki Y., Storch K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashiyaki Y., Storch K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 77
                                                                                                                  Q924Q5
Q924Q5;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2003
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Q9D8L4;
01-JUN-2001
01-JUN-2001
01-MAR-2003
                                                          Mus musculus (Mouse).
                                                                                         VH186.2-D-J-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW;
                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AK007918; BAB25349.1;
HSSP; P01842; 7FAB.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGH-1 OR 1810060009RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APKFQGXATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                            NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGYDYDWFAYWGQGTLVTVSA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDENGDSDY
Eutheria; Rodentia; Sciurognathi;
                        Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. (TrEMBLrel. )
                                                                             (TrEMBLrel. 19, Last see
(TrEMBLrel. 23, Last and
-C mu protein (Fragment)
                                                                                                                                                                             (TrEMBLrel. 19,
                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Rodentia;
                           Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.2%; Score 399; DB 11; 64.7%; Pred. No. 3.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                               Last sequence update)
                                                                                                                                                                                   Created)
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Last annotation updat
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                           143
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067795; BAB63280.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_w.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
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SMART; SM00406; IGV; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Mus musculus (Mouse).
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"Direct Estimation of Relative Affinity by Flow
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"Direct Estimation of Relative Affinity
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                                                                    QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
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14; Mismatches
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Pred. No. 1e-32;
4; Mismatches 26;
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Pred. No. 1e
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Q924R2;
Q1-DEC-2001
01-DEC-2001
01-MAR-2003
KOZONO Y., KOZONO H., AZUMA T.;
"Direct Estimation of Relative Affinity by Flow Cytometr Affinity Maturation of B Cell Antigen Receptors in Respo Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB069913; BAB63929.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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V23-D-J-C MU.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mu protein (Fragment).
                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15361 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.1%;
                                                                                                                                                                                                                                                                                                                                                                                  (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 398;
Pred. No. 1
                                                                                                                                                                                                                                                                                        Sciurognathi;
                                                                                                                                                                                                                                                                                                               Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60739B790FC6AF24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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in Respon
                                                                                                                                   Cytometry Reveals in Response to (4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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Response to (4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140;
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Query Match
Best Local Similarity
Thes 77; Conserve
Search completed: July 30, 2003, 09:42:47 Job time: 91.6792 secs
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Q924R4
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                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

NON TER 145

NON TER 145

SEQUENCE 145 AA; 16081 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE;
NON_TER 1 1 1
NON_TER 142 142
SEQUENCE 142 AA; 15622 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-D-J-C mu protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1. SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                            BMBL; AB067785; BAB63270.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q924R4
                                                                                                                                                                                                                                                                                                                                                                                nterPro; IPR007110; Ig-like.
nterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                               nterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /droxy-3-Nitrophenyl)Acetyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus (Mouse)
                                                            61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSDYDYDYAMDYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGWEAMDYWGQGTSVTVSS 117
                                                                                                                                                1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYE---GYWGQGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                               QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÓVQLÓQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKÓRÞGÓGLEWIGNINÞSNGGTNÝ 60
                                                                                                                                                                                             62.7%; Score 395.5; DB 11; Length 145; ilarity 64.2%; Pred. No. 2.1e-32; Conservative 14; Mismatches 26; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
; 15622 MW;
                                                                                                                                                                                                                                                                16081 MW; ECDB1A135E05B8AA CRC64;
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution.
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

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9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
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Match
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1 Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:

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*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:

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*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:

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Copyright (c) 1993 - 2003 Compugen Ltd.
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      AAE13143
AAB82709
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Humanised antibody
VEGF antagonist an
Antigen-binding pr
VEGF binding relat
VEGF antagonist an
c-plC11 vector hea
KUR binding immuno
Antigen-binding pr
VEGF binding relat
                                                                                                                                                                                                                                                                                                                                      Description
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Fusion protein pIC	AAW82744	20	281	79.6	02.
റ	AAW41394	18	255	.9	02.
	AAW41387	18	120	79.6	502.5
0	AAU76632	23	124	9	03.
Murine COL1 VH cha	AAY39528	20	124	79.8	03.
RSV19 heavy chain	AAR42804	14	116		04.
VH.	AAR24807	13	116		95.
	ABG75594	24	124		06.
Mouse monoclonal a	ABB83941	23	124		06.
	AAR60565	15	124		6.
g e	AAB61960	22	553	۲	11.
u.	AAB85455	22	553	:	11.
i-CEA	AAW73223	20	553	۲	11.
Single chain anti-	AAW11508	18	553	81.1	11.
chain	AAW60770	19	249	:	11.
	AAR60566	15	124		11.
Fv-re	AAU80040	22	556	2	17.
scFv-rearranged ca	AAU97935	22	556	٥.	17.
MFE-23 antibody.	AAR75719	16	270		17.
2A2 monoclonal ant	ABB99635	24	119		ω
Lead binding MAb 1	AAW01586	18	118	85.0	536.5
Anti-p53 monoclona	AAW89173	20	112	5	36.
Single chain antib	AAW60769	19	243	7.	
Murine anti-p53 mo	AAY70787	21	116	7.	54.
Human p53 protein	AAW28492	18	535	8	58.
3 prote	AAW28491	18	535	88.5	83
ric pic	AAE13145	22	136	8	619
VEGF binding relat	ABJ26731	24	240	œ •	624
gen-bind		23	240	8	624
Ħ	AAE25960	23	240	8	624
VEGF binding relat	ABJ26724	24	117	98.9	624
en-bindir	AAU74412	23	117	8	624
anti-KDR	AAE25955	23	\mathbf{r}	8	624
able hea	9723	21	\mathbf{r}	8	624
binding immur	259	23	238	99.0	625
Mouse anti-KDR p1C	AAE25965	23	135	99.4	627

Searched:

on:

ALIGNMENTS

		PR 31.			PN WO								DT 28.	×	AC AAI	,
Witte L, Rafii S;	CORR CORNELL RES FOUND INC.	 31-MAR-2000; 2000US-0540770.	30-MAR-2001; 2001WO-US10504.	11-OCT-2001.	WO200174296-A2.	Chimeric - Mus sp.	Chimeric - Homo sapiens.	human; chimeric.	monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;	tostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic	scular endothelial growth factor receptor; VEGFR; antagonist; tumour;	 Humanised antibody heavy chain fragment.	28-JAN-2002 (first entry)		AAE13143;	AAB13143 standard; Protein; 117 AA.

Result No.

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RESULT 2
AAB82709
ID AAB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
              02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibodies variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody heavy chain frgament used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                             WO200154723-A1.
                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                        vascular endothelial growth factor; angiogenesis; antiangiogenic;
antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for inhitumour cells that are stimulated by a ligation for the growth factor receptor (VEGFR) in mammals
                                                                                                                                                    Region
                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                  Chimeric
                                                                                                                                                                                                                                                             Chimeric
                                                                                                                                                                                                                                                                                              glioblastoma multiforme;
                                                                                                                                                                                                                                                                                                                           tumour; breast carcinoma; lung carcinoma;
                                                                                                                                                                                                                                                                                                                                                                        IMC-1C11; chimeric
                                                                                                                                                                                                                                                                                                                                                                                                     VEGF antagonist antibody IMC-1C11 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB82709 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                               carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity
117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 15; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
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                                                                                                                                                                                                                                                               Mus
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ilarity 100.0%;
Conservative (
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                                                                                                                  /note= "complementarity determining
                                                                                                                                                                   /note= "complementarity determining region
                                                                        note= dcomplementarity determining region
                                                                                                                                                                                     'label= CDR-H1
                                                                                                                                                                                                                                                                                                           ovarian carcinoma; neuroblastoma;
                                                                                                                                       label= CDR-H2
                                                                                                                                                                                                                                                                                                                                                                      antibody; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 117
                                                                                                                                                                                                                                                                                                                                                      growth factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                              melanoma; therapy; heavy chain.
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Pred. No. 1.5e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                      human; antagonist; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibiting the growth of ligand of vascular endoth
                                                                                                                                                                                                                                                                                                                         prostate carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   particularly humans.
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RESULT 3
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Best Local S
Matches 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preventing significant toxicity of the chemotherapeutic agent, The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-IC11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma, glioblastoma multiforme or melanoma (all claiméd).
                                                                                 Antigen-binding protein; cytostatic; angiogenesis vascular endothelial grow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce regression or arrest of the condition while minimising or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of the heavy chain variable region IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating or controlling an angiogenic dependent condition (e.g., neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                   Antigen-binding
                                                                                                                                                                                                                                                        AAU74417 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an
                                                                                                                                                                                      26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 38; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemotherapeutic agent
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                                                               proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                               QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDEENGDSDY
                                                                                                                                                                                                                                                                                                                                           APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGT
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2000US-0539692.
                                                                                                                                                                                      (first entry
                                                                                                                                                   protein heavy chain variable domain
                                                                   inhibitor.
                                                                                                                                                                                                                                                        peptide; 117
                                                                                   growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 631; DB 22; 100.0%; Pred. No. 1.5e-47; tive 0; Mismatches 0;
                                                                                                 antibody heavy chain variable domain; inhibitor; tumour; leukaemia; antibody;
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                                                                                 receptor; VEGF,
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Site located to the N terminus of the CHI domain. (I) is useful for:

C (VEGP) receptor; reducing tumour growth; inhibiting angiogenesis;

CC reducing endothelial cell proliferation; inhibiting ungiogenesis;

CC migration of human leukaemia cells; blocking interaction of a protein and

CC its ligand; promoting interactions between immune cells and target cells;

CC and in vivo and in vitro for investigative, diagnostic or treatment

CC methods. The design of (I) provides for efficient production so that

CC substantially all of the antigen-binding proteins produced are assembled

CC in the desired configuration. (I) is bivalent and bispecific, homogeneous

CC and in tetrameric form. The heavy chain constant domains which constitute

CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural

CC antibody and which provide other antibody functions can be present. There

CC is no requirement for processing in vitro to obtain the complete product.

CC This sequence represents a heavy chain variable domain variable domain

CC and a light chain variable domain in one polypeptide chain, described in
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 61; Page 60; 64pp; English.
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             bispecific antigen-binding
                      Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour;
                                                                                VEGF binding
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                                                                                                                                                                                           ABJ26729 standard; Protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method of the
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                                                                                  related
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                                                                                                                     entry)
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                                                                                  protein
             protein; mouse; murine
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                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 631; DB 23;
Pred. No. 1.5e-47;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
                                Key
                                                                                                                                        IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune diseastumour; breast carcinoma; lung carcinoma; prostate carcinoma;
                                                                                                                                                                                                                                                                                                                    AAB82701 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New bispecific antibodies having antigen-binding sites specific for first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
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N-PSDB; ABT23307.
                                                                                                            glioblastoma multiforme; melanoma; therapy;
                                                                                                                                                                                                                                                        15-OCT-2001
                                                                                                                                                                                                                                                                                        AAB82701;
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                  Peptide
                                                                Chimeric -
                                                                                                                                                                                                                       VEGF antagonist antibody IMC-1C11 heavy chain variable region
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117; Conser
                                                                                                                              carcinoma;
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                                                                             Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA;
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                                                                sapiens
1..19
/label= Signal_peptide
                               Location/Qualifiers
                                                                                                                              ovarian carcinoma;
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                                                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 631; DB 24;
Pred. No. 1.5e-47;
; Mismatches 0;
                                                                                                                              neuroblastoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                          autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a first antigen binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating
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RESULT 6
AAE28916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma system tumour, neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of the heavy chain variable region of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibod or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce regression or arrest of the condition while minimising or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                              QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or controlling an angiogenic dependent condition (e.
                                                                                                       APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS
                                                                                                                                                    APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS
                                                                                                                                                                                                    QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                                                                                                                                                                                                                                                                                                                                              136 AA,
                                                                                                                                                                                                                                                                                                           Conservative
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/label= Mature_protein
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/note= "complementarity determining
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Pred. No. 1.7e-47;
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100.0%; <u>.</u>

Score 631; DB 23; 'Length 136; Pred. No. 1.7e-47; ; Mismatches 0; Indels 0;

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Gaps

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The invention relates to a method of inhibiting tumour growth which CC involves administering, vascular endothelial growth factor receptor (VEGFR) antagonists in combination with radiation, chemotherapeutic cagent, or epidermal growth factor receptor (EGFR) antagonist. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. C tumour of the breast, heart, lung, small intestine, colon, spieen, bone, ckidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, colon marrow, blood, thymus, uterus, testicles, cervix or liver) over cexpresses VEGFR. It is also useful for inhibiting growth of colon tumour crown or small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR. It is preferably useful for treating subjects with both solid tumours, color preferably high vascular tumours and non-solid tumours. The inhibition of two preferably high vascular tumours and non-solid tumours. The inhibition of the progression of tumour growth includes prevention or inhibiting of the correction of tumours, including cancerous and non-cancerous tumours, where the progression of tumours includes the invasiveness, metastasis, cecurrence and increase in size of the tumour. The present sequence is c-plCll vector containing human heavy chain (VH) protein. This sequence is used to illustrate the method of the invention.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-691738/74.
N-PSDB; AAD46315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epidermal growth factor receptor; non-small cell lung carcinoma; breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain;
                                                                                                                                                                                                                                                                                                                                                                     Example 9; Fig 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMCL-) IMCLONE SYSTEMS INC (ROCK/) ROCKWELL P. (GOLD/) GOLDSTEIN N I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2001; 2001US-0798689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c-p1C11 vector heavy chain (VH) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE28916 standard; Protein; 136
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RESULT 7
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Matches 117
                                                                                                                                                                      Sequence
                                                                                                                                                                                                           to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is KDR binding immunoglobulin related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; immunoglobulin; kinase insert domain-containing receptor; KDI foetal liver kinase; FLK-1 receptor; vascular endothelial growth fac VEGF; tumour growth; heavy chain variable region; VH; angiogenesis; p1C11; scFv antibody.
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                                                                                                                                                                                                                                                                                                                              Disclosure; Page 17-18; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (/TTIM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE25963 standard; Protein; 238
                                                                                                                                                                                                                                                                                                   The present invention relates to novel immunoglobulin molecules that
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-589175/63.
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                                                                                 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OVKLOOSGASUVGSGASVKLSCTTSGFNIKDFYMHWVKORPEQGLEWIGWIDPENGDSDY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                   APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS
APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS
                                                        QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
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                                                                                                                 Conservative
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                                                                                                                         Score 631; DB 23;
Pred. No. 3.1e-47;
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RESULT 8
AAU74420
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AAU7
CC complex of two polypeptides (P1) and two second polypeptides (P2) which CC are stably associated in an immunoglobulin like complex. P1 has an CC antigen-binding site located to the N terminus of immunoglobulin (Ig) (CI ight chain constant domain (CI domain), and P2 has an antigen-binding (CI ight chain constant domain of the CH1 domain. (I) is useful for: CC reducing the activation of a vascular endothelial growth factor (VEGF) receptor; reducing the activation, inhibiting anglogenesis; CC reducing endothelial cell proliferation; inhibiting anglogenesis; CC reducing endothelial cell proliferation; inhibiting vEGF induced (CI intro of human leukaemia cells; blocking interaction of a protein and CC its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment (CI substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute (CI the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural cantibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This is the amino acid sequence of a single chain variable fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen-binding protein; single chain variable fragment; svFv; antigen; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 63; Page 62-63; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes an antigen-binding protein (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-2000; 2000US-206749P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  two polypeptides and two second polypeptides
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    claimed in claim 61"
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RESULT 9
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                                                                                                                                                                 The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56-57; 98pp; English
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                          Score 631; DB 24;
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the activation of KDR, for reducing angiogenesis. The present sequence i heavy chain variable region (VH).

anti-KDR

p1C11

SCPV

antibody

The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KOR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting the activation of KDR, for reducing tumour growth and for inhibiting

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RESULT 10
AAE25965
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Peptide
                                            Novel immunoglobulin molecule for reducing tumor growth, lkinase insert domain-containing receptor with an affinity human vascular endothelial growth factor, and neutralizes
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foetal
Disclosure; Fig 4; 34pp; English
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DB; AAD42832.
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liver kinase; FLK-1 receptor; vascular endothelial growth
tumour growth; heavy chain variable region; VH; angiogenesi
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20..135
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determining region 1 (CDR-H1)"
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determining region 2 (CDR-H2)"
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                                                                                                                                        The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is KDR binding immunoglobulin related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR; foetal liver kinase; FLK-1 receptor; vascular endothelial growth fact VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;
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                                                                                                       Sequence
                                                                                                                                                                                                                                                 Disclosure; Page 17-18; 34pp; English.
                                                                                                                                                                                                                                                                                    Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
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WITTE
                                                                                                                                                                                                                                                                                                                                                                                 Witte L;
                                                                Similarity
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               QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
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QVKLQQSGAELVGSGASVKLSCTTSSFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
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Pred. No. 3.8e-47;
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QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60

Query Match Best Local Matches

116;

Conservative

0

Mismatches

DB 21; <u>ب</u>

Length 117; Indels

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Gaps

Similarity

98.9%;

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                                                                                            domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single chain antibody, a diabody, a triabody, a monovalent single chain antibody, a diabody, a triabody, a humanised antibody or a chimerised antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoms multiforme, hemangioblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the immunoglobulins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin; antibody; complementary determing region, complementary determing region, complementary wascular endothelial growth factor; KDR; kinase insert domain containing receptor; multivalent; monovalent; kinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody; glioblastoma multiforme; hemangioblastoma; AIDS; central nervous system neoplasma; AIDS associated Karposi's sarcoma; central nervous system neoplasma; AIDS associated Karposi's sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 50-51; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              used to reduce tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-505966/45.
N-PSDB; AAA53767.
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                                                                                                                                                                                                                                                                                                                                                                       New immunoglobulin molecules are described that bind kinase insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMCL-) IMCLONE SYSTEMS INC
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                                                               117 AA;
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99US-0240736.
Score 624; Db 2.
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ARESULT 13
ARES955
ID ARES5
XX ARES5
AC ARES5
XX DT 15-NC
XX Mouse
KW Mouse
KW Mouse
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XX VEGF;
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                                                                                                                                                                                                                                                                                                                          Matches 116;
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tunour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR plC11 scFv antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                    APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                     APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
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Pred. No. 6e-47;
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                                                                                                                                                                                                                                             CC complex of two polypeptides (PI) and two second polypeptides (PP) which CC complex of two polypeptides (PI) and two second polypeptides (PP) which CC are stably associated in an immunoglobulin like complex. PI has an CC antigen-binding site located to the N terminus of immunoglobulin (Ig) clight chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) clight chain constant domain (CL domain), and P2 has an antigen-binding constant domain (CL domain), and P2 has an antigen-binding constant domain (CL domain), and P2 has an antigen-binding constant domain (CL domain), and P2 has an antigen-binding constant domain (CL domain), and P2 has an antigen-binding constant domain (CL domain), and P2 has an antigen-binding constant domain domain (CL domain), and P2 has an antigen-binding constant domain domain domain and described constant constant domain promoting interactions between immune cells and the design of (I) provides for efficient production go that constant constant domains which constitute constant domains which constitute constant domains which constitute constant domains which constitute 
                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen-binding protein; antibody heavy chain variable domain; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 57; Page 57;
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    APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGT
                                                                                     QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDF
                                                                 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWI
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99.1%;
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Pred. No. 6e-47;
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RESULT 15
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Best Local Simi
Matches 116;
                                                                                                                                                                                                                           The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-201468/19.
N-PSDB; ABT23302.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEGF binding related protein SEQ ID No 7.
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                                                                                                                                                 Local Similarity
 61
                 61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYMGQGTTVTVSS 117
                                                                              1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                               QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY
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99.1%;
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Search completed: July 30, Job time : 118 secs

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Minimum DB
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Perfect score:
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10 US-09-974-051-1
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US-09-798-689-21
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Sequence 23, Appl
Sequence 27, Appl
Sequence 7, Appl
Sequence 29, Appl
Sequence 28, Appl
Sequence 21, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 27, Appli
Sequence 28, Appl
Sequence 27, Appli
Sequence 38, Appl
Sequence 7, Appli
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Sequence 1, Appli
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US-10-259-087A-18	-09-974-516-1		-051-	4-051-		US-09-974-052-9	w	-09-158-1	-809-	US-10-283-349-31	-10-056-794-	-09-910-4	-910-483-	-10-095-4	-252-978-	-10-252-978-1	US-10-165-732A-1	US-09-802-083-1	1	US-09-158-120A-18	-784-	US-09-855-632-11	US-09-963-620-11	-09-934-773-	US-09-854-811-11	US-09-855-153-11	564-329A-	-059-1	US-09-910-059-11
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ALIGNMENTS

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RESULT 1
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Best Local Similarity
Matches 117; Conserv
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SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 23
LENGTH: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER: CEC. 15. NC. 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OP INVENTION: Antibodies Specific to
FILE REFERENCE: 11245/46505
                                                                                                                                                                                                                                                                                                 LENGTH: 11
TYPE: PRT
                                     61
  61
                        APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                          QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                  QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
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Pred. No. 1.2e-51;
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RESULT 2 US-09-865-198-22

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                                                                                                                                                                                                                                        SEQ ID NO 7
LENGTH: 117
TYPE: PRT
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Best Local
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                                                                                                                                                                                                   ORGANISM: Mouse
-09-798-689-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists TITLE OF INVENTION: Combined With Radiation and Chemotherapy FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP CURRENT APPLICATION NUMBER: US/09/798,689
CÜRRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/401,163
PRIOR APPLICATION NUMBER: 09/401,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CÜRRENT APPLICATION NUMBER: US/09/865,198
CÜRRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and MethorITLE OF INVENTION: Production FILE REFERENCE: 11245/47102
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 08/
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SOFTWARE: WordPerfect 8.0 for Windows
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                                                                                                                                         Similarity
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APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
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Goldstein, Neil I.
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Pred. No. 1.2e-51;
Mismatches 0;
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US-09-865-198-28
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; ORGANISM: Mouse
US-09-976-787-29
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                                                                                                                                  Query Match 100.0%; Sest Local Similarity 100.0%; Matches 117; Conservative 0;
                                                                                                                                                                                                                                                         SEQ ID NO 28
LENGTH: 238
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Best Local Similarity
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APPLICANT: Zhu, Zhe
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                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
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SOFTWARE: WordPerfect
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CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
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TITLE OF INVENTION: Antibodies Specific to
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                                                                                                                                                                                                                                           TYPE: PRT
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                                                                QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGT
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100.0%; Pred. No. 2.6e-51;
Live 0; Mismatches 0;
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                                                                                                                                  Score 631; DB 10;
Pred. No. 2.6e-51;
0; Mismatches 0;
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                                 VIVSS 117
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APPLICANY: Goldstein, Neil I.

TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
FIILE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/401,163
PRIOR APPLICATION NUMBER: 09/401,163
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 08/967,113
PRIOR APPLICATION NUMBER: 08/967,113
PRIOR APPLICATION NUMBER: 08/706,804
PRIOR APPLICATION NUMBER: 08/706,804
PRIOR FILING DATE: 1996-09-03
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/326,552
PRIOR FILING DATE: 1995-01-20
PRIOR FILING DATE: 1994-10-20
PRIOR FILING DATE: 1994-10-20
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US-09-976-787-7
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APPLICANT: Witte, Larry
APPLICANT: Witte, Larry
ITILE OF INVENTION: Antibodies Specific to KDF
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR PILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
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; ORGANISM: Mouse
US-09-798-689-21
                                                                                         ; TYPE: PRT ; ORGANISM: Mus musculus US-09-976-787-7
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SEQ ID NO 7
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SEQ ID NO 21
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Best Local Similarity
       Matches 116;
                     Query Match
Best Local Similarity
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                                                                                                                                                        LENGTH: 117
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    Conservative
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                     98.9%;
99.1%;
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  Score 624; DB Pred. No. 5.4e 0; Mismatches
                                          DB 9; Length 117;
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                       4e-51;
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  Indels
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Patent NO. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                            SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 28
LENGTH: 240
TYPE: PRT
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SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 7
                                                                           Matches
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Best Local Similarity
                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to
FILE REFERENCE: 11245/46505
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TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                         116;
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                      QVKLQQSGAELVGSGASVKLSCTTSGENIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
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QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY
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S20020064528A1
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Pred. No. 5.4e-51;
                                                                                            Score 624; DB 9;
Pred. No. 1.2e-50;
                                                                           Mismatches
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RESULT 11
US-09-968-851-38
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US-09-865-198-27
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Publication No. US20020193561A1
GENERAL INFORMATION:
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SEQ ID NO 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
TITLE OF INVENTION: Production
FILB REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR APPLICATION NUMBER: US 60/206,749
RESIDENT PRIOR PRIOR PRIOR PRIOR PRIOR SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 240
TYPE: PRT
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                                                                     APPLICATION NUMBER: US/09/968,851
FILING DATE: 03-OCT-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                        ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CONSEILLER, EMMANUEL
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APPLICATION NUMBER: PCT/FR96/01111 FILING DATE: 17-JUL-1996
                                    APPLICATION NUMBER: US/08/983,035 FILING DATE: 20-Feb-1998
                                                                                                                                                                                                                                                                                                                     STATE: DC
                                                                                                                                                                                                                                                                                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                        DUNNER, LLP
STREET: 1300 I Street, NW
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99.1%;
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Pred. No. 1.2e-50;
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                                                                                                                                                                              Version #1.30
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US-10-032-482-7
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Matches
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APPLICANT: COhen, I
APPLICANT: ROTTER,
                                                                                                                                                                                                                                                                                           SEQ ID NO 7
                                                                                                                                                                                Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: IL 121041
PRIOR FILING DATE: 1997-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/032,482
CURRENT FILING DATE: 2002-01-02
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/09/445,602
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: PCT/IL98/00266
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TITLE OF INVENTION: IMM
FILE REFERENCE: COHEN42
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                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                      ORGANISM: Mus musculus
                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19-JUL-1995 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : HERKEL, Johannes
INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
                                                                                                                                                                                                                                                                                                              PatentIn version 3.0
                                                                    FQGKATMTADTSSNTAYLQLSSLASEDTAVYYCN-FYGDALDYWGQGTTVTVS
                                FOGKATMTADSSSNTAYLOLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVT
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REGISTRATION NUMBER: 47,114
REFERENCE/DOCKET NUMBER: 03804.0142
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Wolkowicz, Roland
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EREZ-ALON, Neta
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                                                                                                                                            Score 536.5; DB 14;
Pred. No. 7.1e-43;
6; Mismatches 6;
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Pred. No. 3.4e-44;
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LENGTH: 124
                                  SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 1
LENGTH: 124
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CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/025,403
PRIOR FILING DATE: 1998-02-18
PRIOR PELICATION NUMBER: PCT US97/19642
PRIOR PILING DATE: 1997-10-30
PRIOR PILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 60/029,694
                                                                                                                PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/029,694
PRIOR FILING DATE: 1996-10-31
                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/974,051
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                      APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal
TITLE OF INVENTION: Antibodies
                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, W.H. Kerr APPLICANT: Tempest, Philip R.
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NUMBER OF SEQ ID NOS: 50
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TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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APPLICANT: Tempest, Philip R.
                                                                                                                                                                                                                                       FILE REFERENCE:
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                                                                                                  NUMBER OF SEQ ID NOS:
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NAME/KEY: Murine Col-1 VH
LOCATION: 1..124
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ORGANISM: Mus musculus
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Local Similarity 76.4%;
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Harris, William J.
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Pred. No. 9.4e-40;
Pred. No. 9.4e-40;
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NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: musculus
FEATURE:
NAME/KEY: Murine Col-1 VH
LOCATION: 1..124
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Publication No.
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Best Local Similarity
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/974,516
CURRENT FILING DATE: 2001-10-09
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APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affin
TITLE OF INVENTION: Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/025,403 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/029,694
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                                                                  61
                                                                                                 61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA-----YYGDYEGYWGQG 110
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                              TTVTVSS 117
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TTVAVSS 124
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Pred. No. 9.4e-40;
8; Mismatches 9;
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version (c) 1993 - 2003
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US-08-672-507-2
US-08-471-426-6
PCT-US94-01709-6
US-08-61-052-16
US-09-364-088-16
US-09-364-088-16
US-09-364-089-16
US-09-171-426-4
PCT-US94-01709-4
US-09-672-609-1
US-09-423-439-26
US-09-423-439-26
US-09-564-329A-11
US-09-564-329A-11
US-09-564-329A-11
US-09-564-329A-11
US-08-348-548-8
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US-08-361-521-44
PCT-US95-01219-44
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2, Appli
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Query Best I	RESULT 1 US-08-983-(Sequence Sequence Patent NO GENERAL CO	. 224676666666666666666666666666666666666
Match Local Simi	TIT 1 1 1 8-983-035A-38 8-983-035A-38 GUERCE 38, Application US/08983035 tent No. 6326464 GENERAL INFORMATION: APPLICANT: CONSEILLER, EMMANU BRACCO, LAURENT TITLE OF INVENTION: P53 PROTE USES THERE NUMBER OF SEQUENCES: 59 CORRESPONDENCE ADDRESS: ADDRESSE: FINNEGAN, HEN COUNTRY: USA ZIF: 20005-3315 COMPUTER READABLE FORM: MEDIUM TYPE: F10ppy disk COMPUTER: IBM PC compati OPERATING SYSTEM: PC-DOS SOFTWARE: Patentin Relea CURRENT APPLICATION NUMBER: US/0 FILING DATE: 20-Feb-1998 CLASSIFICATION NUMBER: PC-PELING DATE: 17-UU-1995 APPLICATION NUMBER: PT-PELICATION NUMBE	471.5 471.5 469 467 467 467 462 462 462 462 462 462 462 462 462 462
larity	A-38 5.226464 1.200 US/0 1.200 US	77777777777777777777777777777777777777
88.5%;	-035A-38 a 38, Application US/08983035A No. 6336464 No. 6336464 AL INFORMATION: APPLICANT: CONSEILLER, EMMANUE APPLICANT: CONSEILLER, EMMANUE APPLICANT: CONSEILLER, EMMANUE BRACCO, LAURENT ITILE OF INVENTION: P53 PROTEI USES THERE USES THERE USES FINNEGAN, HEND DUNNER, LLP STREET: 1300 I Street, NW CITY: Washington STATE: DC COUNTRE READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatib OPERATING SYSTEM: PC-DOS/ SOFTWARE: Patentin Releas CLASSIFICATION NUMBER: US/08 FILING DATE: 10-UUL-1995 APPLICATION NUMBER: FR 95 FILING DATE: 17-UUL-1996 APPLICATION NUMBER: FR 95 FILING DATE: 19-UUL-1996 APPLICATION NUMBER: 47,1 REFERENCE/DOCKET NUMBER: 47,1 RE	20254 2254 226 227 227 227 227 227 227 227 227 227
Score 5 Pred. N	NSEILLER, EMMANUEL ACCO, LAURENT WITON: P53 PROTEIN VARI USES THEREOF ENCES: 59 ADDRESS: E: FINNEGAN, HENDERSON, DUNNER, LLP 1300 I Street, NW shington CS SYSTEM: PC-DOS/MS-DOS SYSTEM: PC-DOS/MS-DOS SYSTEM: PC-DOS/MS-DOS SYSTEM: PC-DOS/MS-DOS CON NUMBER: US/08/983,0 ATION DATA: ION NUMBER: US/08/983,0 ATION LOURL-1996 ION NUMBER: FR 95/08729 ATION DATA: ITON NUMBER: FR 95/08729 ATION LOURL-1996 ITON NUMBER: AT, 114 ATION TORNATION: FRORMATION: FRORMATION: FRORMATION: E: 202-408-4400 2 ID NO: 38: ATTEN MOMBER: 33804. RIPTION: SEQ ID NO: 38: RIPTION: SEQ	PCT-US96-0944 US-08-245-081 US-08-232-081 US-08-561-521 PCT-US95-0121 US-08-822-830 US-08-950-660 US-08-950-660 PCT-US93-0092 US-08-561-521 PCT-US93-0092 US-08-561-521 PCT-US93-092 US-08-792-824 US-08-792-824 US-08-792-824 US-08-792-824
558.5; DB No. 8.2e-4	VARIA SON, \$00, #1.0, 8729 8729 804.0	-09448-18 6-265A-29 2-081B-38 1-521-9 -01219-9 2-830B-13 2-830B-13 2-830B-2 -0-660-2 -0-660-2 -00924-2 1-521-4 -10121-9 1-521-4 -10121-4 -
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Length 535;	THERAPEUTICAL GARRETT &	Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
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US-08-767-128-22
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                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US96/0: FILING DATE: 05-JUN-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/541,373 FILING DATE: 10-OCT-1995
                                HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US96/09258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FASTSEQ Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
ORIGINAL SOURCE:
            FRAGMENT TYPE:
                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
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STREET:
Mir
                                                                                  STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                              NAME: Carter, Charles G. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/462,798 FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
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                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Merchant, Gould, Smith, Edell, Welter & Schmidt
3100 No. 6111079west Center, 90 South Seventh St
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612/332-9081
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US-08-652-507-2
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Patent No.
                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ARTHUR R. Crawford
REGISTRATION UNMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       TELEPHONE: //-- TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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144
                         115 VSS 117
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                                                                                                              61 DPKFQGKATMTADTSSNIAYLQLSSLTSEDTAVYYCNPYGYDDAMDYWGQGTSVTVSS 118
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1 EVQLQQSGAELVRSGASVKLSCTASGENIKDYYMHWVKQRPEQGLEWIGWIDRENGDTEY 60
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VSS 146
                                                       APKFQGKATFTTDTSSNTAYLQLSSLTSEDTAVYYCNEGTPTGPYYFD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                     82.0%;
81.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/652,507
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Pred. No. 2.3e-47
7; Mismatches
                                                                                                                                                                      Score 517.5; DB 2
Pred. No. 5.3e-45;
5; Mismatches 9
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                                                                                                                                                                                                  DB 2;
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                                                                                   MGQGTTVT 114
                                                       GOGTTVT 143
                                                                                                                                            ENGDSDY 60
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RESULT 4
US-08-017-570-6
; Sequence 6, Application US/08017570

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                                                                                                                                                                                                                                                             US-08-471-426-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: AMINO ACID
TOROY COY. 15002
                                                                                                                                                                                                                        Sequence 6, Application US/08471426 Patent No. 5808033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
                                                                                                                                                                                                       GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,570
FILING DATE: 19390216
CLASSIFICATION: 424
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                    TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MEZES, PETER S
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
                               NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS:
                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. E
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                   DDRESSEE:
                                                                                                                                                                                                                                                                                                                                        118 TTVTVSS 124
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                                                                                                                           GOURLIE, BRIAN B
RIXON, MARK W
MEZES, PETER S
KAPLAN, DONALD A
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E: Duane C. U
P.O. Box 1967
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                                                                                                         SCHLOM, JEFFREY
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77.2%;
                   Ulmer
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Pred. No. 8.4e-45;
9; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
FILING DATE: 06-UNN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Applicat:
GENERAL INFORMATION
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Best Local Similarity
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FILING DATE: 16-FEB-1993
ATTORNEY AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34.941
REFERENCE/DOCKET NUMBER: C-38,77
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                  COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01709
FILLING DATE:
CITAGLE TOTALE:
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LENGTH: 124 amino acids
TYPE: amino acid
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APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: A NOTEL FAMILY OF ANTI-CARCINGEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                       COUNTRY: US
ZIP: 48641-1967
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CITY: Midland
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                                                                                                                                                                                                                                                                                                          ADDRESSEE: Duane C.
                       CLASSIFICATION:
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Pred. No. 8.4e-45;
9; Mismatches 7
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Best Local Similarity
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                          INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDLUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (517) 636-8104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yashwant M. Dec
APPLICANT: Joel Goldstein
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                                                                                                                               REFERENCE/DOCKET NUMBER: MX
TOPOLOGY.
                                                                                            TELEPHONE:
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REFERENCE/DOCKET NUMBER:
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            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
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                                                         : (617) 227-5941
(617) 227-5941
TO NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 State Street, Suite 510
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Pred. No. 8.4e-45;
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Patent No. 6
                                                                                            Matches
                                                                                                         Query Match
Best Local (
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                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MX
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02103-10. COMPUTER REALDABLE FORM:
COMPUTER REALDABLE FORM:
COMPUTER REALDABLE FORM:
COMPUTER REALDABLE FORM:
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ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                         Local Similarity
                                                                                                                                                                                      TYPE: am:
TOPOLOGY:
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62 PKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCN-----AYYGDYEGYWGQGTTVTV 115
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                                                                                                                                                                                       amino acid
GY: linear
                              Boston
                                                              VKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDYA 61
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(7) 10 NO: 16:
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                                                                                            Conservative
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VENTION: THERAPEUTIC COMPOUNDS COMPRISED
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                                                                                                                                                                                                                                                                               (617) 227-7400
                                                                                                         81.1%;
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80.3%;
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                                                                                         Score 511.5; DB 3
Pred. No. 5.1e-44;
6; Mismatches 9
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Pred. No. 5.1e-44;
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US-09-364-088-16
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                   RESULT 10
US-09-102-716-16
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   Sequence 16, Application US/09102716
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 07-JUNE-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
APPLICATION NUMBER: US 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                     Local
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80.3%;
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Pred. No. 5.1e-44;
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GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
                                                                                                                                                           Sequence 4. Patent No.
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Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                           GENERAL
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: KAPLAN, DONALD A APPLICANT: SCHLOM, JEFFREY TITLE OF INVENTION: A NOVEL TITLE OF INVENTION: ANTIGEN NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
TYPE: amino acid
TYPE: hinear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/102,716
FILING DATE: 22-Jun-1998
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
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TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
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                                                                                                                                                           4, Application US/08017570 o. 5472693
                                                                                                                                             INFORMATION:
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STATE: Massachusetts
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                                                                                       RIXON, MARK W
MEZES, PETER S
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                                                                                                                         GOURLIE, BRIAN B
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 A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC ANTIGEN CHIMERIC ANTIBODIES
24
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Pred. No. 5.1e-44;
6; Mismatches 9
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RESULT 12
US-08-471-426-4
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APPLICANT: GOURLI
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EILING DATE: 19930216
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REGISTRATION NUMBER: 34,941
                                                                                                                                                                                                            APPLICANT: KAPLAN, DO
APPLICANT: SCHLOM, JI
TITLE OF INVENTION: J
TITLE OF INVENTION: J
TITLE OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acid
      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
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ADDRESSEE: Duane C. U
STREET: P.O. Box 1967
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nes 97; Conserv
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TYPE: AMINO ACID
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Pred. No. 2.7e-44;
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Best Local 8
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,570
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
OLANE CLASSIFICATION:
OLANE CLASSIFICATION:
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OLANE CLASSIFICATION:
OLANG CLASSIFICATION:
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REGISTRATION NUMBER: 34,941

REFERENCE/DOCKET NUMBER: C-38

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                  INFORMATION FOR SEQ ID NO:
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                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 124 amino acic
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ADDRESSEE: Duane C. Ulmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: A NOVEL PAMILY OF ANTI-CARCINOEMERYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
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                                                                                                                                                              TELEPHONE:
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TOPOLOGY:
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Pred. No. 2.7e-44;
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; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-672-609-1
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 1
LENGTH: 124
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US-09-672-609-1
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US-09-025-403A-1
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Best Local S
Matches 97
            Sequence 1, Application US/09025403A
PAtent No. 6417337
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
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Best Local Similarity
Matches 97; Conserv
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APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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   APPLICANT:
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118 TTVAVSS 124
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1 Similarity 76.4%;
97; Conservative
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Harris, William J
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Pred. No. 5.4e-44;
8; Mismatches 9;
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Pred. No. 2.7e-44;
9; Mismatches 8
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SOFTWARE: Microsoft Word
SEQ ID NO 1
LENGTH: 124
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
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Best Local Similarity
                                                                                                                                                                                                                      Matches
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TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/025,403A

CURRENT FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: PCT US97/19642

PRIOR FILING DATE: 1997-10-30

PRIOR FILING DATE: 1997-10-30

PRIOR FILING DATE: 1996-10-31

PRIOR FILING DATE: 1996-10-31
                                                                                                                                                                                                                                                                                                           NAME/KEY: Murine Col-1 VH LOCATION: 1..124
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                                 111 TTVTVSS 117
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                                                                                                         APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA-----YYGDYEGYWGQG 110
TTVAVSS 124
                                                                       APKFQGKATMTTDYSSNTAYLQLSSLTSEDTAVYYCNTRGLSTMITTRWFFD----VWGAG
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Pred. No. 5.4e-44;
8; Mismatches 9
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Search completed: July 30, 2003, 09:38:31 Job time: 38.7043 secs

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Result
No.
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Maximum DB
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: pir2:*
3: pir3:*
4: pir4:*
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Maximum Match 10
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PS0070
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Ig kappa chain V r
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448 81.6 107 2 311119 19 kappa chain 448 81.6 120 2 3,48971 19 kappa chain 447 81.4 107 2 311118 19 kappa chain 446.5 81.3 108 2 338720 19 kappa chain 446.6 81.2 100 2 \$29590 19 kappa chain 446 81.2 108 2 \$29590 19 kappa chain 446 81.2 108 2 \$29581 19 kappa chain 447 80.9 123 2 \$04573 19 kappa chain 448 80.9 123 2 \$05269 19 kappa chain 441 80.3 106 2 PL0082 19 light chain 441 80.3 106 2 PL0082 19 light chain 440 80.1 97 2 \$26341 19 kappa chain 440 80.1 107 2 PT0402 19 light chain 440 80.1 107 2 S11121 19 kappa chain 441 80.3 106 2 PL088 19 light chain 440 80.1 107 2 S11121 19 kappa chain 441 80.3 107 2 PT0402 19 light chain 440 80.1 107 2 S11121 19 kappa chain 441 80.3 107 2 S11121 19 kappa chain 440 80.1 107 2 S11121 19 kappa chain 441 80.3 107 2 PT0402 19 light chain 442 79.4 97 2 PH1085 19 light chain 443 79.4 99 2 \$29585 19 kappa chain	5	44	43	42	41	40	39	38	37	36	35	34.	ω ω	32	<u>ω</u>	30
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kappa kappa kappa kappa kappa kappa kappa kappa light kappa light light light	S29585	PH1085	PT0402	S11121	S26341	PT0398	PL0082	PT0401	S05269	S04573	S29581	S29590	S38720	S11118	A34871	811119
	Ig kappa chain	Ig light chain	Ig light chain	Ig kappa chain	Ig light chain	light	kappa	light	kappa	kappa	kappa	kappa	light		kappa	Ig Kappa chain

ALIGNMENTS

(fragment)

#text_change

21-Jan-2000

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Ig kappa chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0013
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 198
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Recession: PL0013
A;Molecule type: mRNA
A;Residues: 1-140 <CHE>
A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylchc C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: B54378
A;Status: preliminary
A;Molecule type: mENA
A;Residues: 1-106 <AGA>
A;Residues: 1-106 <AGA>
A;Cross-references: GB:S68985; NID:g545746; PIDN:AAB30096.1; PID:g545747
A;Cross-references: GB:S68985; NID:g545746; PIDN:AAB30096.1; PID:g545747
A;Experimental source: spleen and myeloma cell line MOPC 315.43
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
C;Kuperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>
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B54378
G19 light chain V region anti-triplex DNA - mouse (fragme Ig light chain V region anti-triplex DNA - mouse (fragme Ig light chain V region anti-triplex DNA - mouse (fragme Ig Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Accession: B54378
R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
A;Title: Characterization of a new monoclonal antibody the A;Reference number: A54378; MUID:94165109; PMID:7509814
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PL0013
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Matches 99
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Pred. No. 6.5e-35;
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A;Molecule type: mRNA
A;Residues: 1-132 cLEV,
A;Cross-references: EMBL:X14098; NID:g52562; PIDN:CAA32260.1; PID:g736261
A;Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.
J. Exp. Med. 168, 1607-1620, 1988
A;Title: Algernative V kappa gene rearrangements in a murine B cell lymph:
A;Reference number: JL0061; MUID:89035985; PMID:3141553
A;Accession: JL0062
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
S05268
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A2513
A2513
Example chain precursor V region (MRL22) - mouse
Ig kappa chain precursor V region (MRL22) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #
C;Accession: A32513
R;Kofler, R; Strohal, R; Balderas, R.S.; Johnson,
J. Clin. Invest. 82, 852-860, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M20834; NID:g196943; PIDN:AAA38846.1; C;Superfamily: immunoglobulin V region; immunoglobulin homoloC;Keywords: heterotetramer; immunoglobulin F;38-113/Domain: immunoglobulin homology <TMM>
                                                                                                                                                                                                                                                                 A; Reference number:
                                                                                                                                                                                                                                                                   submitted to the EMBL Data A; Reference number: $05267
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A;Title: Immunoglobulin kappa light chain variable region gene complex organization
A;Reference number: A94689; MUID:88331394; PMID:3138286
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F;23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F;38-111/Domain: immunoglobulin homology <IMM>
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                                          Molecule type: mRNA
                                                                                                                                                                                                                                              Accession: S05268
                                                                                                                                                                                                                                                                                                                                  y kappa chain precursor V-J region (38C13-V1) - mouse (fragment) ($pecies: Mus musculus (house mouse)
Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 2
Accession: S05268; JL0062; S03846
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                  Residues: 1-120 <CAR>
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Pred. No. 2.1e-32;
7; Mismatches 4
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Pred. No. 2.1e-34;
1; Mismatches 5
                                                                                                                                                                                                                                                                                        February 1989
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Ig kappa chain V region (F3, anti-AFP) - C;Species: Mus musculus (house mouse) C;Date: 10-Nov-1997 #sequence_revision 23 C;Accession: PC4405 R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C. Chinese Biochem. J. 12, 648-653, 1996 A;Title: Generation of a phage display li A;Reference number: PC4405 A;Recession: PC4405
                                                                       A;Molecule type: mRNA
A;Residues: 1-99 <GOS-
A;Cross-references: GB:>
A;Cross-references: Jumunoglobulin homolocy
C;Keywords: heterotetramer; immunoglobulin
F;8-81/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                      J. Biol. Chem. 266, 2134-2142, 1991
A; Title: Common structural features among monoclonal antibodies
A; Reference number: A38601; MUID:91115823; PMID:1703527
                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision:
C;Accession: D38601
R;Goshorn, S.C.; Retzel, E.; Jemmerson,
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C; Superfamily: i
F; 16-89/Domain:
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                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                   A; Accession: D38601
                                                                                                                                                                                                                    A; Reference number: A38601;
                                                                                                                                                                                                                                                                                                                             Ig kappa chain V region (6A7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
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A; Residues: 1-107 < DEN>
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Matches
                                     Query Match
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Mus musculus (house mouse)
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94.9%;
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87.7%;
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; Score 481; DB
; Pred. No. 2.3e
1; Mismatches
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Pred. No. 2.1e-32;
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Pred. No. 2.1e-32;
9; Mismatches 6
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A;Experimental source: strain Balb/c
A;Rote: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V region (H18-S415) - mouse
C;Species: Musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
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A30562
Ig kappa chain V regions (27.7.2 and 27.4b.2)
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C;Accession: G27887

C;Accession: G27887

C;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

EMBO J. 5, 1577-1587, 1986

A;Title: Structural and functional implications of a restricted A;Reference number: A91043; MUID:86300658; PMID:2427335

A;Accession: G27887
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A; Residues: 1-107 <SIK>
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C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: A30562
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A;Residues: 1-106 <CAT>
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Best Local 3
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SGRGSGTSFSLTISSMEAEDAATYYCHQRSSYPLTFGAGTKLELK 106
                        SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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Pred. No. 6.3e-32;
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No. 9.1e-32;
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R;Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A;Title: Functional immunoglobulin light chain genes are
A;Reference number: A92781; MUID:89310348; PMID:2501443
A;Accession: PS0070
RESULT 11
S26338
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A; Residues: 1-107 < SIK>
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R;Sikder, S.K.; Bord
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C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
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A; Residues: 1-106 < LEV >
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                                                                                                                   SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                   IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF
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                                                                           SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPYTFGGGTKLEIK
                                                                                                                                                         IVLTQSPAIMSASPGEKVIMTCSASSSVSYMHWYQQKSGTSPKRWVYDTSKLASGVPTRF
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Pred. No. 1.3e-31;
1; Mismatches 7
                                                                                                                                                                                                                                                          Score 471; DB 2;
Pred. No. 1.6e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F.; Akolkar,
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Ig kappa chain V region - mouse C;Species: Mis musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision C;Accession: \$26338

13-Jan-1995

#text_change

20-Jun-2000

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RiStark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a
A;Reference number: S26309; MUID:91341421; F

PMID:1908510

acid

interchange

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protein

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F;16-91/Domain: i
F;24-35/Region: c
F;36-50/Region: f
F;51-57/Region: c
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                                                                    A; Molecule type: mRNA
A; Residues: 1-108 <SHID>
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 1-23, Region: framework 1
                                                                                                                                                                                      R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rott J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and A;Reference number: PL0231; MUID:90111618; PMID:2104919
                                                                                                                                                                                                                                                                     Ig kappa chain V region (anti-DNA, 3H9VK) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change C;Accession: PLO278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: $26338
A; Status: preliminary
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;Species: Mus musculus (house mouse)
;Date: 06-Jan-1995 #sequence_revision
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;Residues: 1-105 <STA>
36-50/Region: 51-57/Region:
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                                  complementarity-determining
                                                        immunoglobulin homology
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Pred. No. 4.7e-31;
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Pred. No. 1.9e-31;
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A; Introns: C; Complex: I
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A; Residues: 114-116 <MIL2>
A; Residues: 114-116 <MIL2>
A; Cross-references: GB:S37664; NID:g250215; PIDN:AAB22332.1; PID:g250218
A; Experimental source: BALB/c germ-line
A; Note: sequences extracted from NCBI backbone; partial nucleotide sequence, A; Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBIPE 10682)
A; Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBIPE 10682)
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Experimental source: mRNA clones for anti-phenyloxazolone antibody 6F6 A,Note: the authors translated the codon TTC for residue 8 as Pro and TTC f,Note: the codon given for 1-Met (AGT) is inconsistent with the authors' t R,Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Pernandez, A.; Gherardi, E Eur. J. Immunol. 22, 1627-1634, 1992 at 1. Immunol. 22, 1627-1634, 1992 A,Title: Non-random features of the repertoire expressed by the members of A,Reference number: A49044; MUID:92289826; PMID:1601044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: V(kappa)Ox1
A;Introns: 17/1
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A;Residues: 1-130 <KAA>
A;Cross-references: GB:M27792; NID:g197159
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F;90-98/Region: complementar
F;99-108/Region: framework '
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A;Note: sequence extracted from NCBI backbone (NCBIN:106802,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-25 <MIL>
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RESULT 15 ; PS0071 Ig kappa chain V region (38C13.V8) - mouse C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000 C;Accession: PS0071 R;Levy, S.; Campbell, M.J.; Levy, R. J. Exp. Med. 170, 1-13, 1989 A;Title: Functional immunoglobulin light chain genes are replaced by ongoin A;Reference number: A92781; MUID:89310348; PMID:2501443 A;Recession: PS0071 A;Status: translation not shown A;Residues: 1-106 <lev> C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin A;Residues: 1-106 <lev> C;Superfamily: immunoglobulin homology <-IMM> C;Keywords: heterotetramer; immunoglobulin F;16-89/Domain: immunoglobulin homology <-IMM> Ouery Match B4.3%; Score 463; DB 2; Length 106; Best Local Similarity 86.7%; Pred. No. 7e-31; Matches 91; Conservative 4; Mismatches 10; Indels 0; Gaps Ouery Match Db 2 IULTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKSGTSPKLWIYSTSNLASGVPARF Db 2 IULTQSPAIMSASPGEKVTMTCSASSSVSYMHWFQQKSGTSPKRWIYDTSKLASGVPARF Oy 62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPTPGSGTKLEIK 106 C SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPTPGAFTKLEIK 106 Search completed: July 30, 2003, 09:44:11 Job time: 32.3422 secs</lev></lev>

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Ig kappa chain V-VI r
Mus musculus (Mouse)
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NON TER
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                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                               NCBI_TaxID=10090
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HSSP; P01679; 2FBJ.
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-!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=83271467; PubMed=6877353;

KBARTIANE M., Griffiths G.M., Markham A.F., Milstein C.

"MRNA sequences define an unusually restricted IgG resp

"mRNA sequences define and unusually restricted igg resp

phenyloxazolome and its early diversification.";

Nature 304.320-324(1983)

-I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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Nature 304:320-324(1983).
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Mammalia; Eutheria;
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ween the Swiss Institute of Bioinformatics and the EBurogean Bioinformatics Institute. There are no rest Burogean Bioinformatics Institutions as long as its content by non-profit institutions as long as its content ified and this statement is not removed. Usage by an ities requires a license agreement (See http://www.isb-
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in V-VI region NQ2-48.2.2.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Nature 304:320-324(1983).
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NCBI_TaxID=10090;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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IPR003006; Ig_MHC.
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Mammalia; Eutheria;
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SMART; SM00406; IGv;
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82.2%;
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                                                                                                           Pred. No. 4.50
5; Mismatches
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Pred. No. 4.5e-37;
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-2
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COMPLEMENTARITY-DETERMINING-1.
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ID KV6A MOUSE
AC P01675;
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DT 21-JUL-1986
DT 15-JUL-1999
DE 15 Kappa cha
OS Mus musculus
OC Eukaryota; N
OC MAMMMalia; EN
OX NCBL TaxiDal
RN [1] TaxiDal
RN [1] FI
RN EDLLINE=790
RA RAD D.N., RA
RT FC CAMBON NO.
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RN INTERPOOLATION
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DR INTERPOOLATION
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DR IMPOSITE; PSE
KW IMMUNOSION
FT DOMAIN
                                                                                                                        P01678;
21-JUL-1986
21-JUL-1986
21-JUL-1989
SEQUENCE.
MEDLINE=81054757;
Rudikoff S., Rao I
                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                    NCBI_TaxID=10090;
                                                                                              Mus musculus (Mouse)
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Mammalia; Eutheria;
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ITE; PS50835; IG_LIKE; 1.
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                    Pred. No. ...
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Score 425; DB 1
Pred. No. 9e-37;
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COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
                                                                 Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostômi;
Sciurognathi; Muridae; Murinae; Mus
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 C.P.J.,
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                                                                                                                                      update)
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 Potter M.;
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                                                                                                                                                                                                                                                                                                                                                                                      Length 107;
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                                                                   Euteleostomi;
; Murinae; Mus
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KV6C_MOUSE
ID KV6C_AC P0167
AC AC P168
AC P
                                                                                                                                    SEQUENCE (161.)

MEDLINE-81054757; Pubric.

A Rudikoff S., Rao D.N., Glaudemans

T "Kappa Chain joining segments and structura.

T combining sites.";

Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274 (1980).

RL Proc. Natl. Acad. Sci. U.S.A. T7:4270-4274 (1980).

T MISCELLANEOUS: THE TWO SEQUENCES ARE IDENTICAL.

TANKOUS: THESE CHAINS WERE ISOLATED FROM MY
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Best Local (
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                        InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
InterPro; IPR003596;
Pfam; PF00047; 19; 1
SMART; SM00406; IGV;
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21-JUL-1986 (Rel. 01, Creace
21-JUL-1986 (Rel. 01, Last :
15-JUL-1999 (Rel. 38, Last :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE (TEPC 601).
MEDLINE=79082830; PubMed=103573;
Rao D.N., Rudikoff S., Potter M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rao D.N., Rudikoff S., Pot
"k Chain variable regions
proteins.";
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Mammalia; Eutheria; Rodentia;
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Mus musculus (Mouse).
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Proc. Natl. Acad. 9
-!- MISCELLANEOUS:
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PS50835;
                                                                          IPR007110; Ig-like, IPR003006; Ig_MHC. IPR003596; Ig_v.
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107
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: THIS CHAIN WAS
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IG_LIKE;
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TEPC 601/TEPC 191.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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Pred.
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BY SIMILARI
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structural diversity
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No. 1.1e-36;
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RESULT 11
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Best Local :
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DOMAIN 24
DOMAIN 34
DOMAIN 34
DOMAIN 49
DOMAIN 56
DOMAIN 88
        DOMAIN
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NON TER
SEQUENCE
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SMART; SM00406; IGv; 1.
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PDB; 2FBJ; 15-OCT-90
                                                                                                                                                                                                                                                             "Kappa Chain
combining sit
                                                                                                                                                                                                                                                                              MEDLINE=81054757; PubMed=6776525; Rudikoff S., Rao D.N., Glaudemans
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Mammalia; Eutheria; Rodentia;
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21-JUL-1986 (Rel.
28-FEB-2003 (Rel.
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21-JUL-1986
                                                                                                                                                                                study at 2.6-A resolution.";
Proteins 1:74-80(1986).
                                                                                                                                                                                                          Davies D.R.;
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                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                            ain joining segments sites.";
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region; 3D
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01, Last sequence update)
41, Last annotation update)
VI region J539.
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80.4%;
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                                COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3. COMPLEMENTARITY-DETERMINING-3.
                                                          COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-4.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-1.
                                                                           FRAMEWORK-1
                                                                                                                                                                         WAS
                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                         MYELOMA
                                                                                                                                                                                                  X-ray
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; Murinae; Mus.
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                                                                                                                                                                                                                  Rudikoff S.,
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                                                                                                                                                                                                  diffraction
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                                                                                                                                                                                                                                                                      antibody
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STRAND

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RESULT 12
KV4A_MOUSE
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Best Local S
Matches 83
                                                                                                                                                                                                                                                                                                                                                    P01680;
21-JUL-1986
21-JUL-1986
                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Bithe European Bioinformatics Institute. There are no restues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                 MEDLINE=82115300; PubMed=6799208;
Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
"Two kappa immunoglobulin genes are expressed in the myeloma S107.";
Cell 26:57-66 (1981).

-i- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
NORMAL KAPPA CHAIN S107.
                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-IV region S107B precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAND
HELIX
STRAND
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TURN
STRAND
Pfam;
SMART;
                                                EMBL; J00577; AAA38780.1; -.
EMBL; V00780; CAA24157.1; -.
PIR; A01943; KVMS7B.
HSSP; P01679; 2FBJ.
                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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STRAND
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STRAND
STRAND
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       InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                   KV4A_MOUSE
                                    nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSGSGSGTSYSLTISRMEAEDAATYYCOORSSYP-FTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
107
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31
32
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59
69
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69
69
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                                                                                                                                                                                                                                                                                                             Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.3%;
77.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 408; DB 1;
Pred. No. 4.9e-35;
                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EA30C9A3E903979C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   129
                                                                                                             (See
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                                                                                                            http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                             a collaboration
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                                                                                                            .ch/announce/
                                                                                                                                                      outstation
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                                                                                                                        commercia:
                                                                                                                                  88
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1 DIELTOSPAIMSASPGEKVTITCSASSSV----SYMHWFQQKPGTSPKLWIYSTSNLAS

Matches

73;

Conservative

13;

20;

Indels

Gaps

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RESULT 13

KV3M MOUSE STAN

ID KV3M MOUSE STAN

AC P01665;

DT 21-UUL-1986 (Rel. 0

DT 21-UUL-1999 (Rel. 3

DT 15-JUL-1999 (Rel. 3
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Best Local S
Matches 84
         Query Match
Best Local
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SEQUENCE
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DOMAIN
                                                                                                                                                 SMART:
                                    SEQUENCE
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MEDLINE=79073152; PubMed=103003;
Loh E.,
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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DOMAIN
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DOMAIN
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DOMAIN
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                                                                                                                       Immunoglobulin
DOMAIN
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                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                         PROSITE;
                                                                                                                                                                                             PIR; A01937; KVMS43.
HSSP; P80362; 1WTL.
                                                                                                                                                                                                                Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                 Pfam; PF00047; ig;
SMART; SM00406; IG:
                                                                                                                                                                                                                                                                                                                  Ig kappa chain V-III region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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         Similarity
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                                                                                                                              PS50835; IG_LIKE; bulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTQSPAIMSASPGBKVTITCSASSSV--SYMHWFQQKPGTSPKLWIYSTSNLASGVPARF
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obulin V region; Sign
                                                                                                                                                                                                                                                                                                                                                                                                                       SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                            SGSGSGTSYSLTISSVEAEDDATYYCOOWSGYP--FGSGTKLEIK
                                                                                                                                                                IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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. 38, Last annotation u
-III region PC 7043.
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         68.0%;
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80.0%;
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                                                                                                                                                                                                                                  Loh E., Schi
information
                                    ₩,
Score 373.5;
Pred. No. 1.7e
13; Mismatches
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Pred. No. 1.2e
7; Mismatches
                                                     FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                          FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                            FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG KAPPA CHAIN V-IV REGION S10
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-4.
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                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                    7A5FCB586C306D29
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                                                                                                                                                                                                                             Schilling J., Ho
                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                111
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         1.7e-31;
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.2e-34;
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                 DB 1;
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                                    CRC64;
                                                                                                                                                                                                                                Hood L.E.;
ce immunoglobulin
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                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                             128
                 111;
5
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KV30_MOUSE

KV30_MOUSE

ID KV30 M

R01667

P01667

P01 15-JUL

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KV3L_MOUSI
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Best Local S
Matches 72
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21-JUL-1986
21-JUL-1986
15-JUL-1999
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NON TER
SEQUENCE
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DOMAIN 24
DOMAIN 39
                                                                                    KV3L MOUSE STANDARD; PRT; 111 AA. P01664; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15 Agpa chain V-III region CBPC 101. Mus musculus (Mouse).
                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Sch. "Rearrangement of genetic information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig kappa chain V-III region PC 6308.
Mus musculus (Mouse).
                       rammalia; Eutheria;
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig;
SMART; SM00406; IG
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HSSP; P80362; 1WTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
SEQUENCE
                                                            Eukaryota;
Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
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                                                                                                                                                                                                                                                                                                                                  GIPARFSGSGSGTDFTLNIHPVEBEDAATYYCQQSNEDPWTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                           GVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                  DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYTASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIELTOSPAIMSASPGEKVTITCSASSSV-----SYMHWFQQKPGTSPKLWIYSTSNLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111
111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111
12071 MW;
                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.1%;
64.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 368.5;
Pred. No. 5.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7A4ADE4D6C256D29 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schilling J., Ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Best Local S
Matches 71
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Pfam; Pr00047; 1g; 1.

SMART; SM00406; IGV; 1.

PROSITE; P850835; IG LIKE; 1

PROSITE; P850835; IG LIKE; 1
                                                                                                                      DOMAIN
DISULFID
NON TER
SEQUENCE
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                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                           PIR; A01936; KVMSC1.
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=79012520; PubMed=99744;
McKean D.J., Bell M., Potter M.
"Mechanisms of antibody diversi
                                                                                                                                                                                                                                                                                                 ISSP; P80362;
                   56
13
                                       μ.
                                                          Н
                                                                                          Similarity
           GVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                     DIELTQSPAIMSASPGEKVTITCSASSSV-----SYMHWFQQKPGTSPKLWIYSTSNLAS
GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPYTFGGGTKLEIK 111
                                                                                                                                 1
24
39
54
61
93
102
23
                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                ell M., Potter M.;
antibody diversity: multiple
                                                                                                                                38
53
60
92
101
111
92
                                                                                                                        11964 MW;
                                                                                         66.8%;
                                                                               14;
                                                                                                                                                                                                                                    <u>-</u>
                                                                             Score 366.5; DB
Pred. No. 8.9e-31
4; Mismatches 2
                                                                                                                                                     FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-4.
                                                                                                                                            BY SIMILARITY.
                                                                                                                                                                                  FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                     FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                        E2B1AD98AD965962
                                                                                                 DB 1;
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Search completed: July 30, 2003, 09:45:10 Job time: 16.5515 secs

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Minimum
Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run
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and is
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493
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473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPTREMBL 23:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            July 30, 2003, 09:31:34; Search time 82.0532 Seconds (without alignments) 333.364 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 ,
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549
                                                                                                                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830525 seqs,
    \begin{array}{c} 96.2 \\ 89.2 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88.0 \\ 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
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sp_phage:*
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1 Q8VDD0
1 Q8K1F3
2 Q8K1F1
99U410
1 Q8K1F1
99U410
1 Q9K1F0
1 Q9JU76
1 Q9JU78
1 Q9JU78
1 Q9JU78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ltd
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Q8vdd0 mus musculu
Q8k1f3 mus musculu
Q8k1f1 mus musculu
Q9u410 schistosoma
Q8k1f0 mus musculu
Q9j176 mus musculu
Q9j178 mus musculu
Q9j178 mus musculu
Q9j178 mus musculu
Q920e9 mus musculu
Q920e9 mus musculu
Q92185 mus musculu
Q9117 homo sapien
Q9u178 homo sapien
Q9u170 homo sapien
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Q8r028 mus musculu	Q8R028	11	234	50.5	277.5	Ü
Q8wtu6 homo sapien	Q8WTU6	4	237	51.2	281	4
mus	Q921A6	H	241	52.1	286	Ü
Q9ul80 homo sapien	Q9UL80	4	114	52.9	290.5	Ñ
Q9j174 mus musculu	Q9JL74	11	99	53.3	292.5	ت
Q8k0f8 mus musculu	Q8K0F8	11	239	53.7	295	Ö
Q9jl82 mus musculu	Q9JL82	•	104	54.1	297	Ö
Bru	Q9ERZ9	1	107	54.7	300.5	œ
homo	QSTCDO		239	55.0	302	7
Q8vc55 mus musculu	Q8VC55	11	239	55.4	304	9
	Q9JL80	11	103		308.5	ū
Omo	Q8NEK0	4	239	56.5	310	4
mus	Q8VCI6	H	238	•	314	Ü
Q96pf6 homo sapien	Q96PF6		116	•	315.5	Ñ
	Q925S9	11	127	58.6	321.5	Ξ
	Q99M37	_	238	58.7	322	0
	Q9UL85		109	•	332	Ö
	OFIA80	•	108	60.6	332.5	ã
Q9ul86 homo sapien	Q9UL86		109	•	337	7
	Q920E6	片	109	61.7	338.5	õ
Ö	Q9UL83		108	62.2	•	ິທ
Q9qyf0 mus musculu	Q9QYF0		298	62.4	342.5	4
Q9jl84 mus musculu	Q9JL84		107	62.4		ເມ
mus	Q91WS9	1	233	62.9		Ñ
Q8vcp0 mus musculu	Q8VCP0	H	234	63.3	347.5	μ
8 mus	Q91WF8		234	63.3	347.5	Ö
Q8nek1 homo sapien	Q8NEK1		234	63.3	347.5	φ
	Q9UL81	4.	107	63.4	348	œ
Q9ul79 homo sapien	Q9UL79	4.	108	64.2	352.5	7

ALIGNMENTS

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RESULT 1
Q8K1F2
ID Q8K1
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                                                                                                   Query Match
Best Local S
Matches 101
                                                                                                   PROSITE;
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                       STRAIN-BALB/C; TISSUE-Hyperimmunized spleen;
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul
"Innate proteolytic antibodies: Failed D-VIPase response to the D
entantiomer of VIP and identification of L-VIPase VL domains.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF516283; AAM64201.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         OBKIF2 PRELIMINARY; PRT; 112 AA.

Q8K1F2;
Q1-OCT-2002 (TrEMBLrel. 22, Created)
Q1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1
                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                             [nterPro;
                                                                                                                                                                                                       nterPro;
                                                                                                                                                                                                                                 [nterPro;
                                                                                                                                                                                                                      nterPro;
                                                  101;
                                                             Similarity
            DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                        PS50835;
DIVLTQSPAIMSASPGEKVTITCNASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                                         IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                   IPR003599; Ig.
IPR007110; Ig-like.
                                                                                                   112
112 AA;
                                                 96.2%;
ilarity 95.3%;
Conservative
                                                                                                                                        IG_LIKE;
                                                                                                    11953 MW;
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•
                                                 Score 528; DB
Pred. No. 1.2e
3; Mismatches
                                                                                                   4716B87FADB543ED CRC64;
                                           DB 11,
1.2e-48;
2;
                                                                         Length 112;
                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                   Mus.
                                                                                                                                                                                                                                                                                      11 S.;
                                                 Gaps
60
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음 성

61

PSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106

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OBKLF3
AC OB
DT OO
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ol-MAR-2002 (TrEMBLrel. 20, L. 01-MAR-2003 (TrEMBLrel. 23, L. Anti-MOG ZI2 variable light chanti-MOG KAPPA.
                                                                                                                                                                                                                                                                 QBK1F3;

Q1-QCT-2002 (TrEMBLrel. 22

Q1-QCT-2002 (TrEMBLrel. 22

Q1-MAR-2003 (TrEMBLrel. 22

Q1-MAR-2003 (TrEMBLrel. 22

Anti-VIPase light chain vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 1.

NON TER 134 134

SEQUENCE 134 AA; 14525 MW:
         SEQUENCE FROM N.A.

STRAIN-BALB/C; TISSUE=Hyperimmunized spleen;
Zhou Y. X., Taguchi H., Planque S., Karle S., Nishiyama Y., P
Innate proteolytic antibodies: Failed D-VIPase response to t
entantiomer of VIP and identification of L-VIPase VI domains.
Submitted *MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c;
Chernajovsky Y.;
Submitted (OCT-2001)
                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AJ41633; CAC94866.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                   Q8K1F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Targeting T cells to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVLTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSPKRWIYDTSKLASGVPARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSGSGTSYSLTISSMEAEDAATYYCHORSSYPWTFGGGTKLEIK
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                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14525 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.8%;
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                                                                                                                                                                                                                                                                      22, Created)
22, Last sequence update)
23, Last annotation update)
variable region (Fragment).
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Last annotation update)
chain (Fragment).
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Pred. No. 8e-45;
4; Mismatches
                                                                                                                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFDF8E2236E2D0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 112
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                                                                                                                                                                                                          Euteleostomi; 
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128
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RESULT 5 Q9U410

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Q9U410

PRELIMINARY;

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RESULT 4
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Best Local S
Matches 94
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Best Local
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SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LI
                                                                                                                       NON TER
NON TER
SEQUENCE
                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                     Q8K1F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                              ZTRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y.,
"Innate proteolytic antibodies: Failed D-VIPase response to
entantiomer of VIP and identification of L-VIPase VI domains
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                             InterPro;
InterPro;
                                                                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                              Anti-VIPase light chain variable
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                                                                                                                                                                                                                                     EMBL; AF516284; AAM64202.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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61
                   59
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                                                                              94;
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0; IPR007110; Ig-like.
798003006; Ig_MHC.
796; Ig_v.
                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                   DIELTQSPAIMSASPGEKVTITCSASSSV--SYMHWFQQKPGTSPKLWIYSTŠNLASGVP
                                                                                                                                                                                            ; IPR003599; Ig.
; IPR007110; Ig-like.
; IPR003006; Ig_MHC.
; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK
                   ARFSGSGSGTSYSLTISRMEAEDAATYYCOORSSYPFTFGSGTKLEIK 106
                                       DIVLTQSPAIMSASPGEKVTMTCRASSSVSSSYLHWYQQKSGASPKLWIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSGSGSGTSYSLTISSMEAEDAATYYCQQYHSYPYTFGGGTKLEIK
                                                                                                                        114 AA;
                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                        12162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12017 MW;
                                                                                         86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.9%;
88.7%;
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Last
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                                                                              Score 473; DB 11;
Pred. No. 8.8e-43;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 488;
Pred. No. 2
                                                                                                                        8BD9833DBF3EEFD1 CRC64;
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annotation update)
                                                                                                                                                                                                                                                                                                                                                              region
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region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                 114
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.2e-44;
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                                                                                9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                  Length 114;
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; Murinae; Mus
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108
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Best Local (
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                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., P.
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., P.
Tinnate proteolytic antibodies: Failed D-VIPase response to ti
entantiomer of VIP and identification of L-VIPase VL domains.
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF516285; AAM64203.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003506; Ig.MHC.
InterPro; IPR003506; Ig.MHC.
InterPro; IPR003596; Ig.—v.
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PROSITE;
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SEQUENCE
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Anti-VIPase light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF207620; AAF19434.1;
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schistosoma japonicum.
Submitted (NOV-1999) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Song X.T., Feng Z.Q., Q:
"Amplification, cloning
variable region gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schistosomatoidea; Schistosomatidae; NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 immunoglobulin
                                                                                                                           Pfam; PF00047; 1g; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Pred. No. 1.7e-42;
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01-DEC-2001 (TrEMBLrel. 1
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SEQUENCE
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Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
Anti-myosin immunoglobulin 1
                                                           Mus musculus (Mouse)
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SMART; SM00406; IG:
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InterPro; IPR007110;
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EMBL; AF206030; AAF69328.1; -.
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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Rodentia;
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Sciurognathi; Muridae;
                    Craniata; Vertebrata; Sciurognathi; Muridae;
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Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (ARR-2001) to the EMBL/GenBank/DDBJ dat
EMBL; BC006643; AAH06643.1; -.
Interpro; IPR003110; Ig-like.
Interpro; IPR003006; Ig-MFC.
R Interpro; IPR003596; Ig-v.
R Pfam; PF00047; ig; 2.
R Pfam; PF00047; ig; 2.
R SMART; SM00406; IG-y; 1.
R PROSITE; PS00290; IG-MHC; 1.
SEQUENCE 235 AA; 26021 MW; 5FC73BDEBDSE8FEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                     NON_TER
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                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20448942; PubMed=10992488;
Malkiel S., Liao L., Cunningham M.W.,
"T-Cell-dependent antibody response t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9JL78;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JL78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               streptococcal polysaccharide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A.CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-myosin
                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Infect.
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                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiac myosin."
                                                                                                                                                                                                                                                                                                                                                                                                                              t. Immun. 68:5803-5808(2000).
AF206028; AAF69326.1; -.
P01679; 2FBJ.
63
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                                                                                                                                                                                    Similarity
                       SYSLTISRMEAEDAATYYCQQRSSYP-FTFGSGTKLEIK
                                                                                                 MSASPGEKVTITCSASSSVS--YMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM
                                                                          MAASPGEKITITCSASSSISSNYLHWYQQKPGFSPKLLIYRTSNLASGVPTRFSGSGSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLMIYSTSNLASGVPARF
SYSLTIGIMEAEDVATYYCQQGSSIPRYTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                            IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGSGSGTSYSLTISNMEAEDVATYYCOOWSRNPPTFGVGTKLELK
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101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) (TrEMBLrel. 15, 0) (TrEMBLrel. 15, 1) (TrEMBLrel. 23, 1) (TrEMBLrel. 23, 1) immunoglobulin 1:
                                                                                                                                                               Conservative
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tumor;
                                                                                                                                                                                                                                     101
; 10778 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                73.5%;
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81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Last sequence update)
, Last annotation update)
light chain variable reg
                                                                                                                                                           Score 403.5;
Pred. No. 1.9e
6; Mismatches
                                                                                                                                                             6
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-acetyl-glucosamine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                              0A7F65E6A7E6F14D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFC73BDEBDSE8FEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                  .9e-35;
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                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi; ; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epitope of is cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235;
                                                                                                                                                                                                     101;
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                                                                              62
                                                                                                                    8
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Q8R062
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Q920E9
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Best Local S
Matches 72
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                          Q920E9;
Q920E9;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBRO62;
OBRO62;
O1-JUN-2002
O1-JUN-2002
O1-MAR-2003
                                                                    Submitted (SEP-2000) to the E
EMBL; AF307935; AAL09419.1; -
InterPro; IPR007110; Ig-ilke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB=Colon;

Strausberg R.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ

EMBL; BC027418; AAH27418.1; -

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.
                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LI
                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Cr
01-JUN-2002 (TrEMBLrel. 21, La
01-MAR-2003 (TrEMBLrel. 23, La
14)pothetical 25.9 kDa protein.
Mus musculus (Mouse)
                                                                                                                                Atkin J.D., Iape A., Jenning "Definition of the Idiotope in Mammalian Cells.";
                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                        Pterin-mimicking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 234 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom̃i;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                            (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                               DIELTQSPAIMSASPGEKVTITCSASSSVS-YMHWFQQKPGTSPKLWIYSTSNLASGVPA
                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              RFSGSGSGTSYSLTISRMEAEDAATTYYCQQRSSYPFTFGSGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                               RFSGSGSGTHYSLTISNLEPEDIATYYCQQYSQFPFTFGSGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                        anti-idiotope kappa
                                   IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25857 MW;
                                                                                                                                              Jennings I
diotope of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 371.5;
Pred. No. 1.4e
17; Mismatches
                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                             I.G., Horaitis O., f Pterin-Mimicking
                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostómi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4EB08C81426AEAB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                                                          chain variable
                                                                                                                                                                                                                                                                                                                     111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4e-31;
ches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
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                                                                                                                                                           R.G.
                                                                                                                                                                                                                                                                                                                                                                                127
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12046 MW;

1E46988AA6858526

CRC64;

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RESULT 13
Q9ULT
ID Q9ULT
AC Q9ULT
AC Q9ULT
DT 01-M2
DT 01-M2
DT 01-M2
DT 01-M2
CFrac
CS Homo
OC Bukar
OC Mamma
OC NCBI
RP SEQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPRIVITY
QPR
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Best Local S
Matches 71
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Best Local 6
Matches 72
                                                                                                                                                                                   Q9UL77;
01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9R1A5;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
PROSITE;
NON_TER
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Kappa light chain of Mab7 (Fragment).
Mus musculus 'Marca'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 19; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister r
antibody (Mab 7, its light and heavy chains) and constru
single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF152371; AAD40242.1; -.
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                   Q9UL77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9R1A5
  SEQUENCE
                                                                                                                                                          Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                       NCBI_TaxID=9606;
                                                                                                                                       Fragment).
                                                                                                                 lomo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                    RFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIELTOSPAIMSASPGEKVTITCSASSSV-SYMHWFQQKPGTSPKLWIYSTSNLASGVPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23922 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.0%;
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Pred. No. 2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 362.5; DB 1
Pred. No. 1.1e-30;
                                                                  Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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white pine blister rust monoclonal
chains) and construction of a
                                                                                                                                                                                                                                                                                   108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214
                                                                                             Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata; Euteleostomi;
chi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4e-31
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                                                                    Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
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RESULT 14
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Best Local S
Matches 69
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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q96SA9 PRELIMINARY; PKL; LV. ....
Q96SA9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-BC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa
variable region (Fragment).
                                                                                                                                                                                               PROSITE;
NON_TER
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SEQUENCE
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                                                                                                                                                                                                                                                                  Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
SPROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=98375893; PubMed=9712075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu X., Liu B., Van der Merwe P.L., Young D.C.;
                                                                                                                                                                                                                                                                                                                                          EMBL; U96396; AAB68785.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; "Molecular analysis of polyreactive monoclonal antibodies rheumatic carditis: human anti-N-acetylglucosamine/anti-my
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
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                                 DIELTQSPAIMSASPGEKVTITCSASSSV-SYMHWFQQKPGTSPKLWIYSTSNLASGVPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS50835; IG_LIKE;
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
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108 AA;
                                                                                                                                                                                            107
107 AA;
                                                                                                  Conservative
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                                                                                                                                                                                               11520 MW;
                                                                                                                      64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.7%; Score 360.5; DB 4; 63.6%; Pred. No. 8e-31; tive 20; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lyreactive monoclonal antibodies from anti-N-acetylglucosamine/anti-myosin
                                                                                                  19;
                                                                                               Score 356; DB
Pred. No. 2.4e
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87:184-192(1998).
                                                                                                                                                                                                 4BB43E9C5B577F16 CRC64;
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                                                                                                                      DB 4;
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60

RFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK

В

RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYS-TLTFGGGTKVEIK 106

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RESULT 15
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Search completed: July 30, 2003, 09:42:49 Job time : 84.1643 secs
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                                                                                                                                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SBQUENCE FROM N.A.

MEDLLNE=98277139; PubMed=9614934;

Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clin. Immunol. Immunopathol. 87:184-192(1998). EMBL; AF035036; AAD56272.1; -. HSSP; P80362; IWTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                 59 ARPSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                      61 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108
                                                                                                                                              1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQXPGQAPRLLIYGASSRATGIP 60
                                                                                                                                                               1 DIELTQSPAIMSASPGEKVTITCSASSSV--SYMHWFQQKPGTSPKLWIYSTSNLASGVP 58
                                                                                                                                                                                                                                                                              109 109
109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
A Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution. printed,

4	000	7	6	ហ	4	ω	2	-	Result No.
549	549	549	549	549	549	549	549	549	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match 1
125	108	108	108	108	108	106	106	106	Query Match Length DB
2.2	24	23	23	22	21	24	23	22	:
AAE13146	ABJ26725	AAU74413	AAE25956	AAB82710	AAY97236	ABJ26730	AAU74418	AAE13144	ID
Chimeric picil lig	VEGF binding relat	Antigen-binding pr	Mouse anti-KDR plC	VEGF antagonist an	Variable light cha	VEGF binding relat	Antigen-binding pr	Humanised antibody	Description

WPI; 2001-662942/76

45	44	43	42	41	40	9	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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17	22	22	23	23	20	20	22	22	20	18	16	20	13	22	22	22	20	20	15	22	18	13	18	16	23	22	24	23	23	24	23	23	23	23	22
AAW03182	AAU80040	AAU97935	AAU81278	ABJ10394	AAW82745	AAW82744	AAB61960	AAB85455	AAW73223	AAW11508	AAR75719	AAY34096	AAR21294	AAG63987	AAB82898	AAB82897	AAY28357	AAY28385	AAR53329	AAB83159	AAW41388	AAR21290	AAW41392	AAR79884	AAE28917	AAB70842	ABJ26731	AAU74419	AAE25960	ABJ26732	AAU74420	AAE25963	AAE25961	AAE25966	AAB82702
Guy's 13 anti-Stre	ScFv-rearranged ca	scFv-rearranged ca	μ.	anti-Tac		ein	Bispecific single		ii-CE	Single chain anti-	an		Murine VL kappa gr	Amino acid sequenc	Anti-p53 common mu	Anti-p53 common mu		Anti-GM2 light cha	KM-796 and KM-750	Mouse ganglioside	Anti-CEA antibody	Murine VL kappa gr	Chimeric anti-CEA	ч	c-p1C11 vector lig	۸	VEGF binding relat	Antigen-binding pr	KDR binding immuno	VEGF binding relat	Antigen-binding pr	KDR binding immuno	inding im	~	VEGE antagonist an

ALIGNMENTS

RESULT 1 AAE13144 ID AAE1 (IMCL-) (CORR) Chimeric - Homo sapiens. Chimeric - Mus sp. Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocyti monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse; Humanised antibody light chain fragment. Witte L, 11-OCT-2001. AAE13144; AAE13144 standard; Protein; 106 31-MAR-2000; 2000US-0540770. 30-MAR-2001; 2001WO-US10504. WO200174296-A2 human; chimeric. 28-JAN-2002 (first entry) IMCLONE SYSTEMS INC.
CORNELL RES FOUND INC Rafii S; A.

erythrocytic;

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RESULT 2
AAU74118
ID AAU7
XX AAU7
XX AAU7
XX AAU7
XX AAU7
XX AAU1
XX AAL1
XX AAL1
XX AAL1
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Best Local
New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides -
                                                                                                                               WPI; 2002-106189/14.
N-PSDB; AAU20289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen-binding protein; antibody light chain variable domain; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody light chain fragment used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for inhibiting the growth of non-su tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                       24-MAY-2000; 2000US-206749P
                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2001; 2001WO-US16924.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen-binding protein light chain variable domain (VH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU74418 standard; peptide; 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 16; 68pp; English.
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ilarity 100.0%;
Conservative 0
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Pred. No. 6.4e-32;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC complex of two polypeptides (P1) and two second polypeptides (P2) which CC are stably associated in an immunoglobulin like complex. P1 has an CC antigen-binding site located to the N terminus of immunoglobulin (Ig) Clight chain constant domain (CL domain), and P2 has an antigen-binding Site located to the N terminus of immunoglobulin (Ig) Clight chain constant domain (CL domain), and P2 has an antigen-binding CC site located to the N terminus of the CH1 domain (I) is useful for: CC (NEGF) receptor; reducing tumour growth; inhibiting angiogenesis; CC reducing endothelial cell proliferation; inhibiting angiogenesis; CC migration of human leukaemia cells; blocking interaction of a protein and clits ligand; promoting interactions between immune cells and target cells; CC and in vivo and in vitro for investigative, diagnostic or treatment complete cells; complete configuration. (I) is bivalent and bispecific, homogeneous complete configuration. (I) is bivalent and bispecific, homogeneous can in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural containbody and which provide other antibody functions can be product. There is no requirement for processing in vitro to obtain the complete product. There is no requirement for processing in vitro to obtain the complete product. There is no requirement for processing in vitro to obtain the complete product. There is no requirement for processing in vitro to obtain the complete product. There is no requirement for processing in vitro to obtain the complete product. There is no requirement for processing in our complete product. There is no requirement for processing in our complete complete product. There is no requirement for processing in our complete complete product. The method of the inventible domain in one polypeptide chain, described in the method of the invention.
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Best Local S
Matches 106
                   WPI; 2003-201468/19.
N-PSDB; ABT23308.
                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; antibody; antigen binding site; leukaemia cell; vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABJ26730 standard; Protein; 106
                                                                                                                                                                   26-JUN-2001; 2001US-301299P
                                                                                                                                                                                                                                                     09-JAN-2003
                                                                                                                                                                                                                                                                                               WO2003002144-A1
                                                                                                                                                                                                                                                                                                                                                                                 bispecific antigen-binding protein; mouse; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGF binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 61; Page 61; 64pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 549; DB 23; 100.0%; Pred. No. 6.4e-32; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĕ
                                                                                                                                                                                                                                                                                                                                                                                                     growth factor; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.
                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF receptor; mitogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 106;
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RESULT 4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-2000
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                           Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor,
                                                                                                                      WPI; 2000-505966/45
N-PSDB; AAA53768.
                                                                                                                                                                                                                                                                                                                                29-JAN-1999;
29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200044777-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin; antibody; complementary determing region VEGF; vascular endothelial growth factor; KDR; kinase insert domain containing receptor; multivalent; mumanised antibody; chimeric antibody; tumour; diabody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variable light chain fragment of anti-SI(KDR) antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY97236 standard; Protein; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-2000; 2000WO-US02180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glioblastoma multiforme; hemangioblastoma; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 54; 98pp; English
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reduce tumour growth
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                                                                                                                                                                                                                                                                                                                                99US-0117726.
99US-0240736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         system neoplasms; AIDS associated deficiency syndrome; AIDS; human.
                                                                                                                                                                                                                                                                        SYSTEMS INC
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Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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6.4e-32;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vascular endothelial growth factor (VEGF). The antibodies neutral KDR activation. The immunoglobulin may be a multivalent single chain antibody, a diabody, a diabody, a diabody, a humanised antibody or a chimerised antibody, a triabody, a humanised antibody or a chimerised antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity a VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes
28-JAN-2000; 2000US-0178791
31-MAR-2000; 2000US-0539692
                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                          Chimeric -
                                                                                                                                                                                                                                                                                                         Chimeric
                                                                                                                                                                                                                                                                                                                                   glioblastoma multiforme; melanoma; therapy;
                                                                                                                                                                                                                                                                                                                                                    colon
                                                                                                                                                                                                                                                                                                                                                                               vascular endothelial growth factor; angiogenesis; antiangiogenic;
antitumour; neoplasm; collagen-vascular disease; autoimmune disea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB82710 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                          29-JAN-2001; 2001WO-US02839
                                                                                                                                                          Region
                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                 tumour; breast
                                                                                                                                                                                                                                                                                                                                                                                                            IMC-1C11; chimeric antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGF antagonist antibody IMC-1C11 light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                            r; preast carcinoma; lung carcinoma; prostate carcinoma; carcinoma; ovarian carcinoma; neuroblastoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK
                                                                                                                                                                                                                                                                                          Homo
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                                                                                                                                                                                       'label= CDR-L2
                                                                                                                                                                                                                                   'label=
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                                                                                                                                                                          "complementarity
                                                                                                                                                                                                                   "complementarity
                                                                                                                              "complementarity determining
                                                                                                                                             CDR-L3
                                                                                                                                                                                                                                   CDR-L1
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                                                                                                                                                                                                                                                                                                                                                                                                          mouse; human; antagonist; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 549; DB 21;
Pred. No. 6.5e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                   determining
                                                                                                                                                                        determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mparable affinity to human The antibodies neutralise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
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                                                                                                                                                                                                                                                                                                                                                                               disease;
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RESULT 6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of the light chain variable region of IMC-IC11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibod or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce
                              30-MAY-2002.
12-OCT-2001; 2001US-0976787.
                                                              US2002064528-A1
                                                                                              Mus musculus
                                                                                                                                                                                                            Mouse anti-KDR plC11 scFv antibody VL region #1
                                                                                                                                                                                                                                             15-NOV-2002
                                                                                                                                                                                                                                                                                                            AAE25956 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUNN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemotherapeutic agent
                                                                                                                         ; immunoglobulin; kinase insert domai. liver kinase; FLK-1 receptor; vascutumour growth; light chain variable; scFv antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIELTOSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                           FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 549; DB 22;
Pred. No. 6.5e-32;
; Mismatches 0;
                                                                                                                                          domain-containing receptor; KD
vascular endothelial growth fa
iable region; VL; angiogenesis;
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RESULT 7
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody
                                      Zhu
                                                                                                                                                                                                                     Antigen-binding protein; antibody light chain variable cytostatic; angiogenesis inhibitor; tumour; leukaemia; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
                                                                                       24-MAY-2000;
                                                                                                                24-MAY-2001; 2001WO-US16924
                                                                                                                                            29-NOV-2001.
                                                                                                                                                                                                                                                                                     Antigen-binding
                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                          AAU74413;
                                                                                                                                                                                                                                                                                                                                                                    AAU74413 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 11; 34pp;
                                                                                                                                                                    WO200190192-A2
                                                                                                                                                                                              ds sn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                              (IMCL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   light chain variable region (VL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (/TTIM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JAN-2000; 2000US-0493539
          2002-106189/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-589175/63
                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNÜASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZHU Z.
WITTE L.
                                                              IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Witte L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSGSGSGTSYSLTISRMĒAEDAATYYCQQRSSYPFTFGSGTKLBIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNEASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                    FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                        2000US-206749P
                                                                                                                                                                                                                                                                                      protein light chain variable domain (VH)
                                                                                                                                                                                                                                                                                                                                                                  peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English:
                                                                                                                                                                                                                                                                                                                                                                    108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 549; DB 23;
Pred. No. 6.5e-32;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                leukaemia; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                               domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 6
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New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of

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RESULT 8 ...
ABJZ6725
ID ABJZ67
XX ABJZ67
XX ABJZ67
XX OL-MAY
XX VEGF b
XX Cytost
KW Cytost
KW Leukae
KW bispec
XX bispec
XX Mus sp
XX bispec
XX b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC antigen-binding site located to the N terminus of immunoglobulin (1g)
CC light chain constant domain (CI domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC reducing the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting ungiogenesis;
CC discipling endothelial cell proliferation; inhibiting ungiogenesis;
CC interpolation of human leukaemia cells; blocking interaction of a protein and comparation of human leukaemia cells; blocking interaction of a protein and comparation of invitro for investigative, diagnostic or treatment comparation. (I) in provides for efficient production so that comparation of (I) provides for efficient production so that comparation of the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural continuous and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a light chain variable domain (VH) incorporated conto Pv, an engineered protein containing a heavy chain variable domain containing a heavy chain, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 106; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; mouse; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABJ26725 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are stably associated in an
                                                                                                                                                                                                                                                                                                                               WO2003002144-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGF binding related protein SEQ ID No 8:
                                                                                                                                                                                                 26-JUN-2002; 2002WO-US20332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 57;
                                                                    (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                 26-JUN-2001; 2001US-301299P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention describes an antigen-binding protein (I) comprising a plex of two polypeptides (P1) and two second polypeptides (P2) which stably associated in an immunoglobulin like complex. P1 has an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSGSGSGTSYSLTISRMEAEDAATYYCOORSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 57; 64pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 549; DB 23;
Pred. No. 6.5e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
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RESULT 9
AAE13146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                  Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
                                                                                                                                                                                                                                                                                             Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric; human; plCll vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
11-OCT-2001.
                                                                                                                                       Region
                                                                                                                                                                       Protein
                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                            Chimeric plC11 light chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE13146 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 49-50; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-201468/19.
N-PSDB; ABT23303.
                                                                          Region
                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE13146;
                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                    . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLMIYSTSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                  Homo sapiens.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                     /note= "Mature chimeric plCll light chain fragment"
43..52
                                                                         /label= CDR_L2
107..115
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                     /label= CDR_L1
                                                                                                                                                                                 /label= Leader_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                         CDR_L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 549; DB 24;
Pred. No. 6.5e-32;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
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30-MAR-2001; 2001WO-US10504

31-MAR-2000; 2000US-0540770.

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RESULT 10
AAB82702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for inhibiting the growth of non-solid cumour cells that are stimulated by a ligand of vascular endothelial crowd the factor receptor (VEGRR) in mammals particularly humans. The method involves treating the mammals with humanised VEGRR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic lymphocytic leukaemia, crythrocytic or monocytic leukaemia, crythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric plCll light chain fragment which is used for the construction of chimeric plCll light chain contains cloned variable light chain (VL) and human kappa light chain constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                       IMC-1C11; chimeric antibody; mouse;
vascular endothelial growth factor;
                  Protein
                                                                                                  Chimeric
                                                                                                                                                                            tumour;
                                                                                                                                                                                          antitumour; neoplasm;
                                                                                                                                                                                                                                                   VEGF antagonist antibody IMC-1C11 light chain variable region
                                                                                                                                                                                                                                                                                        15-OCT-2001
                                                                                                                                                                                                                                                                                                                                                    AAB82702 standard; Protein; 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-662942/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106;
                                                                                                                                            carcinoma; ovarian
lastoma multiforme;
                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                        r endothelial growth factor; angiogenesis; antiangiogenic; ur; neoplasm; collagen-vascular disease; autoimmune disease; breast carcinoma; lung carcinoma; prostate carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Fig 11; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMCLONE SYSTEMS INC
CORNELL RES FOUND II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                  FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                               · Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rafii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
/label= Signal_peptide
20..125
/label= Mature_protein
                                                                Location/Qualifiers
                                                                                                                                                          ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                            melanoma; therapy; light chain.
                                                                                                                                                          carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 549; DB 22;
Pred. No. 7.4e-32;
); Mismatches 0;
                                                                                                                                                          neuroblastoma;
                                                                                                                                                                                                                       human; antagonist; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125;
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AAE25966 ID AAE2 XX

AAE25966 standard;

Protein; 125

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RESULT 11

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                                                                                                                                                                                                                                                                                 The present sequence is that of the light chain variable region of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a consciular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1011. Conditions that can be treated include a neoplasm, a collagen-vascular disease, or an autoimmune disease,
                                                                                                                         Matches 106;
                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                       especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, central nervous system tumour, ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal hadministering a combination of an antiangiogenic molecule and
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                     ovarian carcino neuroblastoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2000;
31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemotherapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-514531/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kerbel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2001; 2001WO-US02839
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                              61
                                                             20
                                                                              1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH26414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUNNYBROOK HEALTH SCI
IMCLONE SYSTEMS INC.
               FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                             DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                                         125
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0178791.
2000US-0539692.
                                                                                                                                                                                         AA,
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/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "complementarity
107..115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "complementarity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
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                                                                                                                                          100.0%;
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                                                                                                                         0,
                                                                                                                         Score 549; DB 22;
Pred. No. 7.4e-32;
; Mismatches 0;
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                                                                                                                                                        Length
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Matches 106
                                                                                                                                                                                  to kinase insert domain-containing receptor (\overline{\text{KOR}}) (a human homologue of mouse foetal liver kinase (\overline{\text{FiK}})-1 receptor) with an affinity comparable to human vascular endothelial growth factor (\overline{\text{VEGP}}) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is mouse anti-KDR plCll scFv antibody light chain variable region (\overline{\text{VL}}).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse;
foetal
                                                                                                                                                                                                                                                                                                                                               Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2002064528-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                        Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2001; 2001US-0976787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE2≅p66;
                                                                                                                                                                                                                                                                               The present invention relates to novel immunoglobulin molecules that
                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2000; 2000US-0493539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse anti-KDR p1C11 scFv antibody VL region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   2002-589175/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin; kinase insert domain-containing receptor; KDR;
liver kinase; FLK-1 receptor; vascular endothelial growth factor;
tumour growth; light chain variable region; VL; angiogenesis;
scFv antibody.
80
                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZHU Z.
WITTE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Witte L;
                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      AAD42833
                                                                 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
               FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                  DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 125
                                                                                                                                                          125
                                                                                                        Conservative
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                                                                                                                                                          AA;
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/note= '
                                                                                                                                                                                                                                                                                                         4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Light chain complementarity
determining region 1 (CDR-L1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Light chain complementarity
determining region 3 (CDR-L3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= Signal-peptide
                                                                                                                                                                                                                                                                                                      34pp;
                                                                                                      100.0%; Score 549; DB 23; 100.0%; Pred. No. 7.4e-32; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mouse
                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p1C11 scFv antibody mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complementarity
2 (CDR-L2)"
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                                                                                                        Indels
                                                                                                                              Length
                                                                                                                               125;
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RESULT 13
AAE25963
ID AAE25
XX
AC AAE25
XX
AC AAE25
XX
DT 15-NC
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Best Local Sim
Matches 106;
                                                                                                                                                                                                                                                                                                                                  to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth attor (VEGP) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is KDR binding immunoglobulin related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR; foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor; VEGF; tumour growth; heavy chain variable region; VH; angiogenesis; p1C11; scFv antibody.
                              AAE25963;
                                                        AAE25963 standard; Protein; 238 AA
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 17-18; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparal human vascular endothelial growth factor, and neutralizes activat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-589175/63.
N-PSDB; AAD42825.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDR binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE25961;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-2000; 2000US-0493539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002064528-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel immunoglobulin molecules that bind
                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                            193
                                                                                                                                                                                133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZHU Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Witte
                                                                                                                                                                                                  DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                                DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                     FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                            FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 238
                                                                                                                                                                                                                                                                                             238 AA;
                                                                                                                                                                                                                                    100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin
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                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                 Score 549; DB 23;
Pred. No. 1.3e-31;
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and neutralizes activation
                                                                                                                                                                                                                                                                23;
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                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                   238;
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                                                                                                                                                                                                                                      Gaps
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15-NOV-2002

(first entry)

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RESULT 14
AAU74420
ID AAU74
XX AU74
XX AAU74
XX AATig
CX AV74
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KW CYCOE
KW CSCOE
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Best Local (
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                                                                                                            cytostatic;
vascular end
cell prolife
Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is KDR binding immunoglobulin related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse;
foetal
                                                                                                                                                                                                                                                                                               Antigen-binding
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                                                                                                                                                                                                                             Antigen-binding
                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU74420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-589175/63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (/TTIM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2002
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                                                                                                                proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liver kinase; FLK-1 tumour growth; heavy scFv antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZHU Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                            ic; angiogenesis inhibitor; tumour; leukaemia;
endothelial growth factor receptor; VEGF;
liferation inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
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                                                                                                                                                                                                                         protein; single chain variable fragment; svFv; antigen;
                                                                                                                                                                                                                                                                                               protein, single chain variable fragment version #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 549; DB 23;
Pred. No. 1.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain-containing receptor; KDR; vascular endothelial growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain-containing
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                                                                                                                                                                           CC complex of two polypeptides (PI) and two second polypeptides (P2) which CC are stably associated in an immunoglobulin like complex. PI has an CC antigen-binding site located to the N terminus of immunoglobulin (Ig) (Site located to the N terminus of immunoglobulin (Ig) (C) site located to the N terminus of the CHI domain. (I) is useful for: CC returnising the activation of avascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; CC reducing endothelial cell proliferation, inhibiting vEGF induced (C) migration of human leukaemia cells; blocking interaction of approtein and CC and in vivo and in vitro for investigative, diagnostic or treatment (C) and in vivo and in vitro for investigative, diagnostic or treatment (C) in the design of (I) provides for efficient produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous in the desired configuration. (I) is bivalent and bispecific, homogeneous can be region (e.g., CH2 and CH3 for an 1gG molecule) of a natural (C) antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. (ScFv), an engineered procein containing a variable light and variable for interaction on one polypeptide, described in the method of the
                                                                                                                               Query Match
Best Local Similarity
                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New bispecific immunoglobulin-like antigen-binding protein tumour growth and for inhibiting angiogenesis, comprises a two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Region
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 193
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                FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK
                                                  DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "15 amino acid linker joins the VH and regions of the single chain variable protein. Encoded by AAS20285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= VH
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                                                                                                                               100.0%;
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Pred. No. 1.3e-31;
                                                                                                                 Mismatches
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RESULT 15

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                                                                                                                                    Query Match 100.0%; Score 549; DB 24; Best Local Similarity 100.0%; Pred. No. 1.3e-31; Matches 106; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                       The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 56-57; 98pp; English.
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                                                                      133 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
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                     61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                         1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 238
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Result
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-865-198-28

US-09-798-689-21

US-09-76-787-28

US-09-865-198-27

US-09-910-059-17

US-09-910-059-9

US-10-247-488-4

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                 Sequence 24, Appl
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Sequence 29, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 27, Appli
Sequence 4, Appli
Sequence 4, Appli
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    Sequence
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ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Witte, Larry
APPLICANT: Witte, Larry
ITILE OF INVENTION: Antibodies Specific to KD;
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILLING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR PILING DATE: 2000-01-28
PRIOR PILING DATE: 1090-01-29
PRIOR FILING DATE: 1999-01-29
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                                                                                                                                                                                                                                                      ; ORGANISM: Mouse US-09-976-787-24
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US-09-976-787-24
                                                                                                                                                                                                                                                                                              SEQ ID NO 24
LENGTH: 106
TYPE: PRT
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                                                                                                                                                                  Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                     61
19
                          FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTTFGSGTKLEIK 106
                                                                                                          DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                           DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                100.0%; Score 549; DB 9; ilarity 100.0%; Pred. No. 5.8e-40; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                          Length 106;
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RESULT 2 US-09-865-198-23

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; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined with Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
PAIOR APPLICATION NUMBER: 00/401,163
PAIOR APPLICATION NUMBER: 08/967,113
PAIOR FILING DATE: 1999-09-22
PAIOR APPLICATION NUMBER: 08/967,113
PAIOR APPLICATION NUMBER: 08/967,113
PAIOR APPLICATION NUMBER: 08/967,013
PAIOR APPLICATION NUMBER: 08/476,533
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Patent No.
                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1994-1
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1994-0
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER:
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NUMBER OF SEQ ID NOS: 34
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PRIOR APPLICATION NUMBER: US 60/206,749
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CURRENT FILING DATE: 2001-05-24
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                                                                                                                                                                                                                                     ORGANISM: Mouse
                                                                                                                                                                                                                                                          TYPE: PRT
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61 R#GSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                     23, Application US/09865198
5. US20020103345A1
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                                           DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
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                                                                                                                           Score 549; DB 11;
Pred. No. 5.8e-40;
); Mismatches 0;
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Pred. No. 5.8e-40;
; Mismatches 0;
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US-09-865-198-8
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APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US Patent No. US20020103345A1
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
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TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/477102
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SOFTWARE: WordPerfect
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PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
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CURRENT FILING DATE: 2001-10-12
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ORGANISM: Mus musculus
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                                                        FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                           DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
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FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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                                                                                                                                                                                                                                                                                                                        Score 549; DB 10;
Pred. No. 5.9e-40;
); Mismatches 0;
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; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28
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RESULT 8
US-09-798-689-21
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SEQ ID NO 29
LENGTH: 238
TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. US20020103345A1 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Production FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR PILING DATE: 2000-05-24
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
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APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                          133 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 192
                                                                                                           61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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                                                                              FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 238
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                                                                                                                                                                                                                                          100.0%; Score 549; DB 10; 100.0%; Pred. No. 1.3e-39; tive 0; Mismatches 0;
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Pred. No. 1.3e-39;
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APPLICANT: Goldstein, Neil I.

APPLICANT: Goldstein, Neil I.

TITIE OF INVENTION: Method for Reducing Timor Growth with VEGF Antagonists
IIILE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/401,163
PRIOR FILING DATE: 1997-09-22
PRIOR APPLICATION NUMBER: 08/967,113
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 08/967,13
PRIOR APPLICATION NUMBER: 08/96,804
PRIOR APPLICATION NUMBER: 08/96,533
PRIOR APPLICATION NUMBER: 08/476,533
PRIOR APPLICATION NUMBER: 08/326,552
PRIOR APPLICATION NUMBER: 08/326,552
PRIOR APPLICATION NUMBER: 08/326,552
PRIOR APPLICATION NUMBER: 08/326,552
PRIOR APPLICATION NUMBER: 08/196,041
PRIOR PRIOR DATE: 1994-10-20
PRIOR PRIOR DATE: 1994-10-20
PRIOR APPLICATION NUMBER: 08/196,041
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US-09-976-787-28
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SEQ ID NO 21
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Best Local Similarity
                                                                                      Matches 106;
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                                                                                                                                Query Match
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APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to
FILE REFERENCE: 11245/46505
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TYPE: PRT
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TYPE: PRT
                                                                                                        Local Similarity
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D. US20020064528A1
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DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
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ilarity 100.0%;
Conservative 0
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                                                                                   Score 549; DB 9;
Pred. No. 1.3e-39;
0; Mismatches 0;
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Pred. No. 1.3e-39;
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US-09-910-059-17
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; ORGANISM: Mouse
US-09-865-198-27
  Best Local Similarity
                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
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Best Local :
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Patent No. US200
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APPLICANT: Zhu, Zhe
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CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-04-29
PRIOR APPLICATION NUMBER: GB 9703103.3
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                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
NUMBER OF SEQ ID NOS: 131
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CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Emery, Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
TITLE OF INVENTION: Their Therapeutic use in an Adept System
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SOFTWARE: WordPerfect 8.0 for Windows
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                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                  FEATURE: OTHER INFORMATION: chimaeric light chain sequence
                                                                                                                                                                     LENGTH: 235
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S20020103345A1
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  97.3%;
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Score 534; DB 10;
Pred. No. 2.4e-38;
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Pred. No. 1.3e-39;
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US-09-910-059-9
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CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR PILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: CET/GB97/01165
PRIOR PILING DATE: 1997-04-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-05-04
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                Sequence 2, Application US/10247488 Publication No. US20030022244A1 GENERAL INFORMATION:
                                                               SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
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LENGTH: 108
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                                                                                                                               CURRENT APPLICATION NUMBER: US/10/247,488
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/526,738
PRIOR FILING DATE: 2000-03-16
                                                                                                                                                                                                                   APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53 FILE REFERENCE: 1196336-RAMOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Copley, Clive G
APPLICANT: Edge, Michael Derek
APPLICANT: Emery, Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA,
TITLE OF INVENTION: Their Therapeutic use in ar
FILE REFERENCE: 1991-209
                                                                                                          NUMBER OF SEQ ID NOS:
ORGANISM: Humanus
                    LENGTH: 256
TYPE: PRT
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les 101; Conservative
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Pred. No. 1.7e-38;
4; Mismatches 1;
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US-10-247-488-4
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                                                        CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/187,595
PRIOR APPLICATION NUMBER: PCT/US01/07193
PRIOR APPLICATION NUMBER: PCT/US01/07193
PRIOR APPLICATION NUMBER: 00/315,943
PRIOR APPLICATION NUMBER: 60/315,943
PRIOR APPLICATION NUMBER: 60/349,830
PRIOR APPLICATION NUMBER: 60/349,830
PRIOR APPLICATION NUMBER: 60/394,741
PRIOR APPLICATION NUMBER: 60/394,741
                                                                                                                                                                                                                                                                                                                                                        Publication:
GENERAL INFORMATION:
APPLICANT: Abrahamson, Julie A.
APPLICANT: Bochner, Bruce
APPLICANT: Erickson-Miller, Connie L.
APPLICANT: Kikly, Kristine K.
APPLICANT: Kikly, Tochert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10247488 Publication No. US20030022244A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10232187 Publication No. US20030092091A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 101; Conservative
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Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/526,738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53 FILE REFERENCE: 1196336-RAMOT
                                                                                                                                                                                                                                                    FILE REFERENCE: GH50042-1
CURRENT APPLICATION NUMBER: US/10/232,187
CURRENT FILING DATE: 2002-08-29
                                                                                                                                                                                                                                                                                                        APPLICANT: Schleimer, Robert
APPLICANT: Nulku, Turkan E.
TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 258
TYPE: PRT
ORGANISM: Humanus
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                                         LING DATE:
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Windows Version 4.0
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                                                                                                                                                                                                      SEQ ID NO 4
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                        Query Match
Best Local Similarity 95.3
Matches 101, Conservative
61
               61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                              1 DIELTOSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                            EIILTOSPAIMSASPGEKVSITCSATSSVSYMHWFOOKPGTSPKLWIYSTSNLASGVPVR 60
FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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                                                                                                                           Score 526; DB 15;
Pred. No. 5.3e-38;
3; Mismatches 2;
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Search completed: July 30, 2003, 10:20:30 Job time: 130.299 secs

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Maximum
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Maximum Match 100%
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Perfect score:
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Issued Patents AA:*

1 (cgn2=6/ptodata/1/iaa/5A COMB.pep:*

2 (cgn2=6/ptodata/1/iaa/5B COMB.pep:*

3 (cgn2=6/ptodata/1/iaa/6A COMB.pep:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	υ	4.	u	2	1	Result No.
516	516	516	516	516	516·	516	516	516	516	516	516	516	518	518	521	521	523	523	523	523	523	529	529	529	532	534	Score
94.0	•	94.0	٠	٠	94.0	٠	94.0	•	94.0	94.0	94.0	94.0	94.4	94.4	94.9	94.9	٠	٠	٠	95.3	5	9	96.4	96.4	96.9	97.3	Query
106	106	106	106	106	106	106	106	106	106	106	106	. 106	105	105	666	281	553	553	553	553	270	129	129	129	108	235	Length
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49,		49,	e 163,	e 163,	16,	Sequence 1, Appli	16,	Ļ	Sequence 16, Appl	,	16	Sequence 1, Appli	12	12	Sequence 51, Appl	44,	16,	16,	16,	16	ν	9	N	2	е 9	Sequence 17, Appl	Description

Sequence 9, Application US/09171945
Patent No. 6277599

GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

Emery, Stephen Copley, Clive Graham Edge, Michael Derek

516 94.0 106 2 US-08-082-042A-83 516 94.0 106 3 US-08-839-765-163 516 94.0 106 3 US-08-839-765-163 516 94.0 106 3 US-08-484-337-1 516 94.0 106 3 US-08-484-337-1 516 94.0 106 4 US-09-610-838-163 516 94.0 239 3 US-08-279-772A-8 516 94.0 239 3 US-08-902-486-11 516 94.0 239 3 US-08-902-486-11 516 94.0 239 1 US-08-463-163-3 498 90.7 144 4 US-09-318-786-2 499 90.7 144 9 US-09-318-786-2 490 89.1 128 3 US-08-919-393-385B-111 489 89.1 128 3 US-08-519-491-2 489 89.1 128 5 PCT-US95-07302-2 481 87.6 246 1 US-08-553-497A-20 481 87.6 246 1 US-08-453-420-3	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	
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US-08-082-842A-83 US-08-883-765-163 US-08-883-765-163 US-08-484-537-1 US-08-484-537-16 US-08-484-537-16 US-08-484-537-16 US-08-163-163-3 US-08-279-772A-8 US-08-279-772A-8 US-08-92-185-113 US-08-92-185-113 US-08-93-385B-111 US-08-93-385B-111 US-08-93-93-385B-111 US-08-93-93-385B-111 US-08-55-497A-20 US-08-211-202-3 US-08-211-202-3 US-08-211-202-3 US-08-211-202-3	μ	Н	N	υ:	ω	4	4	4	Ц	ω	w	4	w	w	ω	ω	N	ŧ
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	57, Appl	, Appli	20, Appl	, Appli	, Appli	111, App	113, App	29, Appl	, Appli	ll, Appl	, Appli	163, App	6, Appl	, Appli	163, App	163, App	83, Appl	1000

LIGNMENT

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; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: humanized US-09-171-945-17
RESULT 2
US-09-171-945-9
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NUMBER OF SEQ ID NOS:
SOFTWARE: PATENTIN Ve:
SEQ ID NO 17
LENGTH: 235
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US-09-171-945-17
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Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT FAILING DATE: 1998-10-29
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR TILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR PILING DATE: 1996-05-04
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                     83
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                                                                                                                                                                       23 DIELTOSPAIMSASPGEKVTITCSASSSVTYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                            FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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                                                                                     FSGSGSGTSYSLTISRMEAEDAATYYCQQRSTYPLTFGAGTKLEIK 128
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Copley, Clive Graham
                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                              97.3%;
96.2%;
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Pred. No. 2.2e-40;
3; Mismatches 1
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                                                                                                                                                                                                                                                                                                   Length 235;
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US-09-171-945-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 583047
                                                                                                                                                                                                                                                             COUNTAL COUNTAL COUNTAL COUNTAL COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
THE COMPANY PC-DOS/MS-DOS
TOTAL COUNTAL COUNTAIN PC-DOS/MS-DOS
TOTAL COUNTAIN PC-DOS/MS-DOS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System FILE REFERENCE: Monoclonal Antibody to CEA CURRENT APPLICATION NUMBER: US/09/171,945
CÜRRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR APPLICATION NUMBER: DET/GB97/01165
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SOFTWARE: PatentIn Ver.
                   TELEFAX: (703)816-410 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
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                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                              TELÉPHONE:
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                                                                                                                                                                                    FILING DATE: 07-SEP-
CLASSIFICATION: 424
                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/116,778E
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VENTION: HUMANIZED ANTIBODIES
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HANAI, NOBUO
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KOIKE, MASAMICHI
                                      (703)816-4100
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                                                            (703)816-4000
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Pred: No. 1.4e-40;
4; Mismatches 1
                                                                                                                                                                                                                                                                      Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                              ADDRESSEE: NIXON & V
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TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
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LOCATION: -22..-1
                                                                                                               ZIP: 22201-4714
                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                               CITY: ARLINGTON
                                                                                                                                                                                STREET:
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APPLICATION NUMBER:
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24..33
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US/08/438,562
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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                                Version
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Best Local :
                                                                                                                                                Sequence 92, Application US/08483528B Patent No. 5939532
                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
               APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUWANIZED ANTIBODIES
                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: domain
LOCATION: 88.96
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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PRIOK;APPLICATION DATA:
APPLICATION UNMER: 08/116,778
FILING DATE: 07-SEP-93
NUMBER
                                                                                                                 APPLICANT:
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LOCATION: 49..55
IDENTIFICATION METHOD:
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LOCATION: 24..33
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OF SEQUENCES:
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                                                            NAKAMURA, KAZUYASU
KOIKE, MASAMICHI
SHITARA, KENYA
HANAI, NOBUO
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103
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Pred. No. 3.2e-40;
1; Mismatches 2;
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RESULT 6
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Sequence 2, Application US/08652507
Patent No. 5876691
GEMERAL INFORMATION:
APPLICANT:
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CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US,
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LOCATION: 24..33
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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ZIP: 22201-4714
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LOCATION:
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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3.2e-40;
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RESULT 7
US-08-661-052-16
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08661052
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APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDÎUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE; Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 117-211
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS;
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                     APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-PC RECEPTOR ANTIBODIES
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APPLICATION NUMBER: US/01
FILING DATE: 02-Jul-1996
CLASSIFICATION: 530
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MEDIUM TYPE: Floppy disk
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NAME: Arthur R. Crawford
REGISTRATION WIMPER: 25
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TOPOLOGY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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T: 1100 No. 5876691th Glebe Road, 8th Floor
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97.1%;
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US/08/661,052
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Pred. No. 2.4e-39;
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; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-661-052-16
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                    REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MX:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (FILING DATE:
                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109-1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: MX
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553 amino acids
                                                    (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chezian Somasundaram
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THERAPEUTIC COMPOUNDS COMPRISED OF ANTI-FC RECEPTOR ANTIBODIES
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97.1%;
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Pred. No. 5.2e-39;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                       Version
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RESULT 9
US-09-364-088-16
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Best Local Similarity 97.1%;
Matches 100; Conservative
                                                                                                                                  Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                       TELEFAX: (617)742-741.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
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TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                     NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MX:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUNE-199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-JUNE-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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475
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                 64 SGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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                                                                                    4 LTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSG
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6365161
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SGSGTSYSLTISRMEAEDAATYYCQQRSSYPLTFGAGTKLELK 517
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28 State Street, 24th Floor
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(617)742-7414
777 TD NO: 16:
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ilarity 97.1%;
Conservative
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                                                                                                                                 Score 523; DB
Pred. No. 5.2e
2; Mismatches
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Pred. No. 5.2e-39;
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                                                                                                                                                                 DB 4;
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                                                                                                                                                               Length 553;
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TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-102-716-16
RESULT 11
US-09-423-439-44
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US-09-102-716-16
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                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                               Query Match
Best Local
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INFORMATION FOR SEQ ID NO: 16:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/102,716
FILING DATE: 22-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MX:
TELECOMMUNICATION INFORMATION:
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: LAHIVE & COCKFIELD
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TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
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                                                                            475
                                                                                                                                                   415 LTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSG
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                                                                                                  SGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                            SGSGTSYSLTISRMEAEDAATYYCQQRSSYPLTFGAGTKLELK 517
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 553 amino acids
TYPE: amino acid
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TELEFAX: (617)227-5941
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                                                                                                                                                                                                                         Score 523; DB 4;
Pred. No. 5.2e-39;
2; Mismatches 1
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Sequence 44, Application US/09423439 Patent No. 6339070 GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles BLAKEY, David Charles

TITLE OF INVENTION: CHEMICAL COMPOUNDS
MUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.:
STREET: 1100 New York Ave., N.W.

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RESULT 12
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APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
APPLICATION NUMBER: GB 9709421.3
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                               APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   SOFTWARE: MS Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, I
STREET: 1100 New York Ave., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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100; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/423,439 FILING DATE: 09-No. 6339070-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20005
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95.2%;
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Pred. No. 3.8e-39;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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US-08-434-000A-12
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Patent No. 6046037
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Best Local Similarity
Matches 100; Conserv
                                                                                                       TELEX: SEQUENCE LISTING INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,
FILING DATE: 12/30/94
                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           TELEPHONE: (619) 552-8400
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ANDREW C. HIATT, JULIAN APPLICANT: K.-C. MA, THOMAS LEHNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                            TELEPHONE: (619) 552-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                    STRANDEDNESS:
                                                                                                                                         TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
   TOPOLOGY:
                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 IVLTQSPAIMSASPGEKVTITCSASSSVTYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 SGSGSGTSYSLTISRMEAEDAATYYCOORSTYPLTFGAGTKLEIK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08434000A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 666 amino acids
                                                                  105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
 DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             storage
                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBULING CONTAINING PROTECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM P.C.
                                                                                                                                                                                                                                                                                         1: including application
1: described below:
08/367,395
                                                                                                                                                                                                                                                                                                                                                                                                        US/08/434,000A
                                                                                                                                                                                                                              34,613
                                                                                                                                                                                                              212/127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 521; DB 4;
Pred. No. 9.5e-39;
3; Mismatches 2
Guy's 13 Kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOS 5.0
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94.4%;

Score 518;

DB 3;

Length 105;

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DESCRIPTION: GO

SEQUENCE DESCRIPTION: SEQ ID NO:

US-09-312-157-12
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Patent No. 6303341
GENERAL INFORMATION:
                                                                                                                                         Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches & 98; Conservative
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                                                                                                                                                                                                                                                                                                                             SEQUENCE LISTING INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ANDREW C. HIATT, JULIAN K.-C. MA, THOMAS LEHNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/434,000 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION PROTECTION PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
   13
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                                                                                        1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWLYSTSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFIFGSGTKLEI 105
                                                                                                                                                                                                                                                          LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSGSGSGTSYSLTISRMEAEDAATYYCHQRTSYPYTFGGGTKLEI 105
                                                                    DIVMTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWLYSTSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.
                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-351
                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 552-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09312157
                                                                                                                                         Conservative
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                                                                                                                                                         94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      storage
                                                                                                                                       Score 518; DB 4;
Pred. No. 2.4e-39;
4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.4e-39;
4; Mismatches 3;
                                                                                                                                                                                                                                              Guy's 13 Kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOS 5.0
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-:
                                                                                                                                                                       Length 105
                                                                                                                                       Indels
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                                                                                                                                       Gaps
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US-07-634-278-1
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION *1.24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
DEFERENCE/DOCKET NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/07634278 Patent No. 5530101
                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: us
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COELINGH, KATHIES APPLICANT: SELICK, Harold E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                     NAME/KEY: Protein LOCATION: 1..106 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
             62
                                              98;
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SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                       : 106 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CO, Man Sung
SCHNEIDER, William
LANDOLFI, Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHNEIDER, William P. LANDOLFI, Nicholas F. COELINGH, Kathleen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QUEEN, Cary L.
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                           . protein
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                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                            94.0%;
                                                                                                                                                                                                                   /note= "Variable region of the mouse
anti-Tac antibody light chain."
                                                                                                                           4.
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                                                                                                                           Score 516; DB 1; Length 106; Pred. No. 3.7e-39; Indels 4; Mismatches 3; Indels
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                                                                                                                           Gaps
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62

SGSGSGTSYSLTISRMEAEDAATYYCHORSTYPLTFGSGTKLELK 106

Search completed: July 30, 2003, 09:38:32 Job time: 35.1595 secs

Page 8